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L10: Entry 2 of 11

File: PGPB

Jun 17, 2004.

DOCUMENT-IDENTIFIER: US 20040115767 A1

TITLE: Immunogenic cell surface proteins of helicobacter pylori

Detail Description Paragraph:

[0073] Cell binding factor 2 (HP0175) has a similarity to cell-binding factor 2 of C jejuni (antigen PEB4A) and is a homologue to Escherichia coli survival protein surA. Here two were identified, but a further two-three isoforms with lower pI's could be proposed with the same M.sub.rs. Cross reactivity with serum from a C. jejuni infected patient was not observed.

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☐ 1. 5874300. 13 Mar 95; 23 Feb 99. Campylobacter jejuni antigens and methods for their production and use. Blaser; Martin J., et al. 435/325; 435/252.3 435/252.31 435/252.33 435/254.2 435/254.21 435/320.1 435/348 435/362 435/365 435/367 435/69.3 536/23.7. C12N015/31 C12N015/63 C12N015/70 C12N015/79.

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☐ 2. 5470958. 16 Sep 94; 28 Nov 95. Antisera against a PEB1 antigen from Campylobacter jejuni. Blaser; Martin J., et al. 530/389.5; 424/164.1 435/252.1 435/7.32 435/822. A61K035/16 A61K039/106.

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☐ 3. 5200344. 13 Nov 90; 06 Apr 93. Diagnostic testing for Campylobacter jejuni or Campylobacter coli infections using novel antigens. Blaser; Martin J., et al. 435/7.32; 435/29 435/7.92 435/961 435/967 436/547 530/389.5. G01N033/569.

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Genes Dev. 1996 Dec 15;10(24):3170-82.

[Related Articles, Links](#)

**SurA, a periplasmic protein with peptidyl-prolyl isomerase activity, participates in the assembly of outer membrane porins.**

**Rouviere PE, Gross CA.**

Department of Stomatology, University of California, San Francisco 94143-0512, USA.

Little is known about either the process of periplasmic protein folding or how information concerning the folding state in this compartment is communicated. We present evidence that SurA, a periplasmic protein with peptidyl-prolyl isomerase activity, is involved in the maturation and assembly of LamB. LamB is a trimeric outer membrane porin for maltodextrins as well as the bacteriophage lambda receptor in *Escherichia coli*. We demonstrate that SurA is involved in the conversion of unfolded monomers into a newly identified intermediate in LamB assembly, which behaves as a folded monomer. The absence of SurA blocks the assembly pathway and leads to accumulation of species prior to the folded monomer. These species also accumulate when the stress sigma factor sigmaE is induced by LamB overexpression. We suggest that accumulation of species prior to the generation of folded monomer is a stress signal sensed by sigmaE.

PMID: 8985185 [PubMed - indexed for MEDLINE]

Mol Microbiol. 1996 Aug;21(4):871-84.

[Related Articles](#), [Links](#)**New components of protein folding in extracytoplasmic compartments of *Escherichia coli* SurA, FkpA and Skp/OmpH.****Missiakas D, Betton JM, Raina S.**

Centre Medical Universitaire, Departement de Biochimie Medicale, Geneve, Switzerland.

A global search for extracytoplasmic folding catalysts in *Escherichia coli* was undertaken using different genetic systems that produce unstable or misfolded proteins in the periplasm. The extent of misfolding was monitored by the increased activity of the sigma E regulon that is specifically induced by misfolded proteins in the periplasm. Using multicopy libraries, we cloned two genes, *surA* and *fkpA*, that decreased the sigma E-dependent response constitutively induced by misfolded proteins. According to their sequences and their biochemical activities, SurA and FkpA belong to two different peptidyl prolyl isomerase (PPI) families. Interestingly, *surA* was also selected as a multicopy suppressor of a defined *htrM* (*rfaD*) null mutation. Such mutants produce a defective lipopolysaccharide that is unable to protect outer membrane proteins from degradation during folding. The SurA multicopy suppression effect in *htrM* (*rfaD*) mutant bacteria was directly associated with its ability to catalyse the folding of outer membrane proteins immediately after export. Finally, Tn10 insertions were isolated, which led to an increased activity of the sigma E regulon. Such insertions were mapped to the *dsb* genes encoding catalysts of the protein disulphide isomerase (PDI) family, as well as to the *surA*, *fkpA* and *ompH/skp* genes. We propose that these three proteins (SurA, FkpA and OmpH/Skp) play an active role either as folding catalysts or as chaperones in extracytoplasmic compartments.

PMID: 8878048 [PubMed - indexed for MEDLINE]



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# UniProtKB/Swiss-Prot entry P56112

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*Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.*


## Entry information

Entry name	<b>Y175_HELPY</b>
Primary accession number	<b>P56112</b>
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 35, November 1997
Sequence was last modified in	Release 35, November 1997
Annotations were last modified in	Release 47, May 2005
<b>Name and origin of the protein</b>	
Protein name	<b>Hypothetical protein HP0175 [Precursor]</b>
Synonyms	None
Gene name	OrderedLocusNames: HP0175
From	Helicobacter pylori (Campylobacter pylori) [TaxID: 210]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.

## References

### [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

**STRAIN**=26695 / ATCC 700392;**DOI**=10.1038/41483; PubMed=9252185 [NCBI, ExPASy, EBI, Israel, Japan]

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G., , Venter J.C.;  
 "The complete genome sequence of the gastric pathogen Helicobacter pylori.";  
 Nature 388:539-547(1997).

## Comments

- **SIMILARITY:** Belongs to the ppiC/parvulin rotamase family.

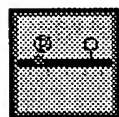
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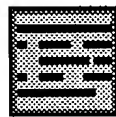
## Cross-references

EMBL	AE000538; AAD07245.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	G64541; G64541.	
HSSP	P39159; 1JNS. [HSSP ENTRY / PDB]	
TIGR	HP0175; -. IPR000297; Rotamase.	

InterPro	Graphical view of domain structure.
Pfam	PF00639; Rotamase; 1. Pfam graphical view of domain structure.
PROSITE	PS01096; PPIC_PPIASE_1; 1. PS50198; PPIC_PPIASE_2; 1. PROSITE graphical view of domain structure (profiles).
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOGENOM	[Family / Alignment / Tree]
BLOCKS	P56112.
ProtoNet	P56112.
ProtoMap	P56112.
PRESAGE	P56112.
DIP	P56112.
ModBase	P56112.
SWISS-2DPAGE	Get region on 2D PAGE.
UniRef	View cluster of proteins with at least 50% / 90% identity.

**Keywords****Complete proteome; Hypothetical protein; Isomerase; Rotamase; Signal.****Features**

Feature table viewer



Feature aligner

Key	From	To	Length	Description
SIGNAL	1	21	21	Potential.
CHAIN	22	299	278	Hypothetical protein HP0175.
DOMAIN	154	253	100	Ppic.

**Sequence information**

Length: **299 AA** [This is the length of the unprocessed precursor]  
 Molecular weight: **34031 Da** [This is the MW of the unprocessed precursor]

CRC64: **E65F3F2F94B11F5A** [This is a checksum on the sequence]

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MKKNILNLAL VGALSTSFLM AKPAHNANNA THNTKKTDS SAGVLATVDG RPITKSDFDM

      70           80           90          100          110          120
IKQRNPNFDF DKLKEKEKEA LIDQAIRTA VENEAKTEKL DSTPEFKAMM EAVKKQALVE

     130          140          150          160          170          180
FWAKKQAEV  KKVQIPEKEM QDFYNANKDQ LFKVQEAHAR HILVKTEDEA KRIISEIDKQ

     190          200          210          220          230          240
PKAKKEAKFI ELANRDTIDF NSKNAQNGGD LGKFQKNQMA PDFSKAAFAL TPGDYTKTPV

     250          260          270          280          290
KTEFGYHIIY LISKDSPVTY TYEQAKPTIK GMLQEKLFQE RMNQRIEELR KHAKIVINK

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P56112 in FASTA  
format

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**BLAST**

BLAST submission on  
ExPASy/SIB  
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,  
Compute pI/Mw, PeptideMass, PeptideCutter,  
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-  
MODEL



NPSA Sequence analysis  
tools



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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the [online BLAST help](#).  
If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 299 AA (of which 8% low-complexity regions filtered out)

Date run: 2005-06-08 04:55:01 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

1,974,938 sequences; 640,866,274 total letters

UniProt Release 5.1 consists of: Swiss-Prot Release 47.1 of 24-May-2005: 181821 en  
TrEMBL Release 30.1 of 24-May-2005: 1748002 entries

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#### List of potentially matching sequences

Send selected sequences to

☐ Include query sequence

Db	AC	Description	Score	E-value
<input checked="" type="checkbox"/>	sp	<a href="#">P56112</a> Y175_HELPY Hypothetical protein HP0175 precursor [HP01...	534	e-150
<input type="checkbox"/>	sp	<a href="#">Q92MQ7</a> Y175_HELPJ Hypothetical protein JHP0161 precursor [JHP...	523	e-147
<input type="checkbox"/>	tr	<a href="#">Q7VJY7</a> _HELHP Hypothetical protein [HH0105] [Helicobacter hepa...	225	1e-57
<input type="checkbox"/>	tr	<a href="#">Q7M902</a> _WOLSU CELL BINDING FACTOR 2 MAJOR ANTIGEN PEB4A [WS128...	184	3e-45
<input checked="" type="checkbox"/>	sp	<a href="#">Q46105</a> CBF2_CAMJE Cell binding factor 2 precursor (Major anti...	138	1e-31
<input type="checkbox"/>	tr	<a href="#">Q5HVH4</a> _CAMJR Major antigenic peptide PEB4 [CJE0699] [Campylob...	138	1e-31
<input type="checkbox"/>	tr	<a href="#">Q8YJG0</a> _BRUME PEPTIDYL-PROLYL CIS-TRANS ISOMERASE [BMEI0123] [...	134	3e-30
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<input type="checkbox"/>	tr	<u>Q8DG31</u>	_VIBVU	Parvulin-like peptidyl-prolyl isomerase [VV10018...	<u>72</u>	1e-11
<input type="checkbox"/>	tr	<u>Q67K72</u>	_SYMTH	Putative post-translocation molecular chaperone ...	<u>72</u>	1e-11
<input type="checkbox"/>	sp	<u>Q8CXK4</u>	PRSA_OCEIH	Foldase protein prsA precursor (EC 5.2.1.8)...	<u>72</u>	2e-11
<input type="checkbox"/>	tr	<u>Q9KQT0</u>	_VIBCH	Peptidyl-prolyl cis-trans isomerase D [VC1918] [V...	<u>72</u>	2e-11
<input type="checkbox"/>	sp	<u>Q81GY5</u>	PRSA1_BACCR	Foldase protein prsA 1 precursor (EC 5.2.1...	<u>71</u>	2e-11
<input type="checkbox"/>	tr	<u>Q8EG15</u>	_SHEON	Peptidyl-prolyl cis-trans isomerase D [ppiD] [Sh...	<u>71</u>	3e-11
<input type="checkbox"/>	tr	<u>Q7MMG3</u>	_VIBVY	Parvulin-like peptidyl-prolyl isomerase [VV1108]...	<u>71</u>	3e-11
<input type="checkbox"/>	tr	<u>Q82SU8</u>	_NITEU	PpiC-type peptidyl-prolyl cis-trans isomerase (E...	<u>70</u>	4e-11
<input type="checkbox"/>	tr	<u>Q7NUZ4</u>	_CHRVO	Probable peptidyl-prolyl cis-trans isomerase (EC...	<u>70</u>	5e-11
<input type="checkbox"/>	tr	<u>Q73CC1</u>	_BACC1	Protein export protein prsA (EC 5.2.1.8) [prsA] ...	<u>70</u>	5e-11
<input type="checkbox"/>	tr	<u>Q88KI6</u>	_PSEPK	Peptidyl-prolyl cis-trans isomerase D, putative ...	<u>70</u>	7e-11
<input type="checkbox"/>	tr	<u>Q6APJ9</u>	_DESPS	Related to peptidyl-prolyl cis-trans isomerase D...	<u>69</u>	9e-11
<input type="checkbox"/>	tr	<u>Q72L30</u>	_THET2	Probable peptidyl-prolyl cis-trans isomerase (EC...	<u>69</u>	9e-11
<input type="checkbox"/>	tr	<u>Q65RG0</u>	_MANSM	SurA protein [surA] [Mannheimia succiniciproduce...	<u>69</u>	1e-10
<input type="checkbox"/>	sp	<u>Q81QT1</u>	PRSA3_BACAN	Foldase protein prsA 3 precursor (EC 5.2.1...	<u>68</u>	2e-10
<input type="checkbox"/>	tr	<u>Q9CJM0</u>	_PASMU	Hypothetical protein PM1979 [PM1979] [Pasteurell...	<u>68</u>	2e-10
<input type="checkbox"/>	tr	<u>Q6HJ34</u>	_BACHK	Protein export protein prsA (EC 5.2.1.8) [prsA] ...	<u>68</u>	2e-10
<input type="checkbox"/>	tr	<u>Q65PE9</u>	_BACLD	YacD [yacD] [Bacillus licheniformis (strain DSM ...	<u>68</u>	2e-10
<input type="checkbox"/>	tr	<u>Q63BM5</u>	_BACCZ	Protein export protein (EC 5.2.1.8) [prsA] [Baci...	<u>68</u>	2e-10
<input type="checkbox"/>	tr	<u>Q8H704</u>	_PHYIN	Peptidylprolyl isomerase [Phytophthora infestans...	<u>68</u>	2e-10
<input type="checkbox"/>	tr	<u>Q72D64</u>	_DESVH	Peptidyl-prolyl cis-trans isomerase domain protei...	<u>68</u>	3e-10
<input type="checkbox"/>	tr	<u>Q62ZT8</u>	_BACLD	Putative PpiC-type peptidyl-prolyl cis-trans iso...	<u>68</u>	3e-10
<input type="checkbox"/>	sp	<u>Q71ZM6</u>	PRSA1_LISMF	Foldase protein prsA 1 precursor (EC 5.2.1...	<u>67</u>	4e-10
<input type="checkbox"/>	sp	<u>Q92BR2</u>	PRSA1_LISIN	Foldase protein prsA 1 precursor (EC 5.2.1...	<u>67</u>	4e-10
<input type="checkbox"/>	sp	<u>Q02473</u>	PRSA_LACPA	Foldase protein prsA precursor (EC 5.2.1.8)...	<u>67</u>	5e-10

## Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs  
([Help](#)) (use ScanProsite for more details about PROSITE matches)

Profile hits	PPIC_PPIASE_2
Pfam hits	Rotanase

Submission	Matches on query sequence											Mat
	1	50	100	150	200	250						1
Y175_HELPY	=====											=====
Y175_HELPJ	=====											=====
Q7VJY7	=====											=====
Q7H902	=====											=====
CBF2_CAMJE	=====											=====
Q5HVV4	=====											=====
Q8YJG8	=====											=====
Q8FYE8	=====											=====
Q57AV6	=====											=====
Q98G68	=====											=====
Q74H76	=====											=====
Q6NCG1	=====											=====
Q92MJ8	=====											=====
Q8XNR4	=====											=====
Q97H89	=====											=====
Q89XV8	=====											=====
Q899G4	=====											=====
Q5FQC9	=====											=====
Q8UA55	=====											=====
Q7CSN8	=====											=====
Q607H8	=====											=====
Q6SF25	=====											=====
Q74RE7	=====											=====
Q5HYH3	=====											=====
PRSA_CLOTE	=====											=====
Q6G5U1	=====											=====
Q6G8Q7	=====											=====
Q82UR3	=====											=====
Q5UF85	=====											=====
PRSA_THETN	=====											=====
Q7NTX8	=====											=====
Q62JM3	=====											=====
Q63V26	=====											=====
PRSA2_BACCR	=====											=====
Q7P917	=====											=====
PLP_RICPR	=====											=====
Q6HN18	=====											=====
PLP_RICCN	=====											=====
Q63EK8	=====											=====
Q738Y8	=====											=====
Q68HG8	=====											=====
Q74H77	=====											=====
Q7WCX5	=====											=====
PRSA_BACHD	=====											=====
PRSA2_BACAN	=====											=====
Q8XYL4	=====											=====
Q7H5E8	=====											=====
Q7VTH9	=====											=====
Q74BG7	=====											=====
Q7NTX1	=====											=====
Q5LNL7	=====											=====
Q5P6R8	=====											=====
Q5L289	=====											=====
Q87R77	=====											=====
Q6HHN3	=====											=====
Q68BE4	=====											=====
Q4ZVM3	=====											=====
Q9I2T8	=====											=====
PRSA2_LISMF	=====											=====
PRSA2_LISIN	=====											=====
Q5HHU3	=====											=====
Q8XYP3	=====											=====
PRSA4_BACCR	=====											=====
Q87YS8	=====											=====
Q5QYK3	=====											=====
Q6SHE5	=====											=====
Q65LT4	=====											=====
PRSA2_LISMO	=====											=====
PPID_HAEDU	=====											=====
Q5NYD2	=====											=====
Q7NTM9	=====											=====
PRSA1_BACAN	=====											=====
Q6HMC8	=====											=====
PRSA_BACSU	=====											=====
Q63EV9	=====											=====
Q8DG31	=====											=====
Q67K72	=====											=====
PRSA_OCEIH	=====											=====
Q9KQT8	=====											=====
PRSA1_BACCR	=====											=====
Q8EG15	=====											=====
Q7MMG3	=====											=====
Q82SU8	=====											=====
Q7NUZ4	=====											=====
Q73CC1	=====											=====
Q88KI6	=====											=====



## Alignments

sp P56112 Hypothetical protein HP0175 precursor [HP0175] 299  
 Y175\_HELPY [Helicobacter pylori  
 (Campylobacter pylori)] AA  
align

Score = 534 bits (1375), Expect = e-150  
 Identities = 275/299 (91%), Positives = 275/299 (91%)

Query: 1 MKKNILNLALVGALSTSFLMXXXXXXXXXXXXXXXXXXXXSSAGVLATVDGRPITKSDFDM 60  
 MKKNILNLALVGALSTSFLM DSSAGVLATVDGRPITKSDFDM  
 Sbjct: 1 MKKNILNLALVGALSTSFLMAKPAHNANNATHNTKTTDSSAGVLATVDGRPITKSDFDM 60

Query: 61 IKQRNPNFDFDKLXXXXXXALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE 120  
 IKQRNPNFDFDKL ALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE  
 Sbjct: 61 IKQRNPNFDFDKLKEKEKEALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE 120

Query: 121 FWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180  
 FWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ  
 Sbjct: 121 FWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180

Query: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAFAFALTPGDYTKTPV 240  
 PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAFAFALTPGDYTKTPV  
 Sbjct: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAFAFALTPGDYTKTPV 240

Query: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK 299  
 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK  
 Sbjct: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK 299

sp Q9ZM07 Hypothetical protein JHP0161 precursor [JHP0161] 299  
 Y175\_HELPJ [Helicobacter  
 pylori J99 (Campylobacter pylori J99)] AA  
align

Score = 523 bits (1348), Expect = e-147  
 Identities = 268/299 (89%), Positives = 272/299 (90%)

Query: 1 MKKNILNLALVGALSTSFLMXXXXXXXXXXXXXXXXXXXXSSAGVLATVDGRPITKSDFDM 60  
 MKKNILNLALVGALS SFLM D+SAGVLATVDGRPITKSDFDM  
 Sbjct: 1 MKKNILNLALVGALSASFLMAKPAHNANNSTHNTKETTDASAGVLATVDGRPITKSDFDM 60

Query: 61 IKQRNPNFDFDKLXXXXXXALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVE 120  
 IKQRNPNFDFDKL ALI+QAIRTALVENEAK EKL+ TPEFKAMMEAVKKQALVE  
 Sbjct: 61 IKQRNPNFDFDKLKEKEKEALIEQAIRTALVENEAKAEKLNQTPEFKAMMEAVKKQALVE 120

Query: 121 FWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180  
 FWAKKQAEVKK+QIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ  
 Sbjct: 121 FWAKKQAEVKKIQIPEKEMQDFYNANKDQLFVKQEAHARHILVKTEDEAKRIISEIDKQ 180

Query: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAFAFALTPGDYTKTPV 240  
 PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAFAFALTPGDYTKTPV  
 Sbjct: 181 PKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAFAFALTPGDYTKTPV 240

Query: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK 299  
 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK

Sbjct: 241 KTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOERMNQRIEELRKHAKIVINK 299

tr Q7VJY7 Hypothetical protein [HH0105] [Helicobacter hepaticus] 276 AA  
 Q7VJY7\_HELHP

align

Score = 225 bits (573), Expect = 1e-57

Identities = 121/258 (46%), Positives = 161/258 (61%), Gaps = 1/258 (0%)

Query: 42 AGVLATVDGRPITKSDFDIKQNRPNFDFDKLXXXXXXALIDQAIRTALVENEAKTEKLD 101  
 A ATVDG IT D +++KQ FNF+++KL LI++ I L+ AK EKLD

Sbjct: 20 AKTYATVDGVAITDKDMEILKQSIPNFYNKLSQEKEMLINELINRQLILKAAKQEKLD 79

Query: 102 STPEFKAMMEAVKKQALVEFWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHARH 161  
 ++ E+ + ++K L++ W KKQA + + + +++ Y N+ + F+ QE ARH

Sbjct: 80 TSKEYTDTINSIKDNLIDLWTKKQANSTQVPTMNDALRKIYQENEGE-FIDQEGKARH 138

Query: 162 ILVKTEDEAKRIIASEIDKQPKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAP 221  
 ILVK+E EAK II E+DK KAK EAKTELAN +IDF SE +NGGDLG F++ M P

Sbjct: 139 ILVKSESEAKEIIEKELDKVGKAKAEAKFIELANAKSIDPASKQKNGGDLGVFKRAGMDP 198

Query: 222 DFSKAAFALTPGDYTKTPVKTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOER 281  
 FSKAAF L PG YTK EV T+FGYHIIYL K P Y+ AK I+ ++ + Q

Sbjct: 199 MFSKAAFDLKPGTYTKEPVLTOFGYHIIYLERKSEPKVIPYKDAKKIENSIMQSIQGG 258

Query: 282 MNQRIEELRKHAKIVINK 299

M Q+I+ LR AKI I K

Sbjct: 259 MMQKIQALRAKAKIKITK 276

tr Q7M902 CELL BINDING FACTOR 2 MAJOR ANTIGEN PEB4A [WS1281] 271  
 Q7M902\_WOLSU [Wolinella  
 succinogenes] AA  
align

Score = 184 bits (466), Expect = 3e-45

Identities = 100/255 (39%), Positives = 152/255 (59%), Gaps = 7/255 (2%)

Query: 41 SAGVLATVDGRPITKSDFDIKQNRPNFDFDKLXXXXXXALIDQAIRTALVENEAKTEKL 100  
 SA LA+VDG IT D ++ + P +D+L +++QAI L+ +AK+E +

Sbjct: 21 SAKTLASVDGDEITDKDISVMLRAMPVGSYDQLPEDMQKKVLEQAIERKLLAKQAKSEGI 80

Query: 101 DSTPEFKAMMEAVKKQALVEFWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHAR 160  
 ++ EFK +E K+ +E W ++Q K + E +M+ FY+ NK++ + A+

Sbjct: 81 QNSKEFKDALEDAKEDLTLEVWMRQOMNNAK---VSEGDMRKIFYDENKEKFKVQPELVKAK 137

Query: 161 HILVKTEDEAKRIIASEIDKQPKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMA 220  
 HILV+ E EAK +I+ET K AK KP EIA +IDF QNGG+LG F K+QM

Sbjct: 138 HILVQNEKEAKEVIAEIGKAG-AKASEKFSKSELAKSIDSIDPAG---QNGGELGWFSKQMV 193

Query: 221 PDFSKAAFALTPGDYTKTPVKTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFOE 280  
 P+P+ AAFAL G Y+KTPVKT+FGYH+IY K + YE KP I+ L+ + F++

Sbjct: 194 PEFANAALQKGSYSKTPVKTOFGYHVIYAEDKKAQAVLPYEDVKPQIEQNLKIQKFRD 253

Query: 281 RMNQRIEELRKHAKI 295

++ ++LR+ A++  
Sbjct: 254 SVSSTAKKLREKAQV 268

sp Q46105 Cell binding factor 2 precursor (Major antigen pab4A) 273  
CBF2\_CAMJE [cbf2] AA  
[Campylobacter jejuni] align

Score = 138 bits (348), Expect = 1e-31  
Identities = 88/256 (34%), Positives = 137/256 (53%), Gaps = 6/256 (2%)

Query: 41 SAGVLATVDGRPITKSDF-DMIKQRNPNFDFDKLXXXXXXALIDQAIRTALVENEAKTEK 99  
+A +ATV+G+ I+ ++ + DF L ALI Q I L+ +AK +  
Sbjct: 20 NAATVATVNGKSISDTEVSEFFAPMLRGQDFKTLPDNQKKALIQQYIMQDLILQDAKKQN 79

Query: 100 LDSTPEFKAMMEAVKKQALVEFWAKKQAEVKKVQIPEKEMQDFYNANKDQLFVKQEAHA 159  
L+ P + ++ K LV + +K +K I +++ FY+ NKD+ A  
Sbjct: 80 LEKDPLYTKELDRAKDAILVNVYQEKILNTIK---IDAAKVKA FYDQNKDKYVKPARVQA 136

Query: 160 RHILVKTEDEAKRII SEIDKQPKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQM 219  
+HILV TE EAK II+E+ + +AKF ELA +IDF SKN GG+LG F ++ M  
Sbjct: 137 KHILVATEKEAKDIINELKGLKGKELDAKFSELAKEKSIDPGSKN--QGGELGWFDQSTM 194

Query: 220 APDFSKAAAFALTPGDYTKTPVKTEFGYHIIYLISKDSPVTTYTYEQAKPTIKGMLQEKLFQ 279  
F+ AAEAL G T TEVKT EGYR+I + + +++ K I+ L+ + F+  
Sbjct: 195 VKPFTDAAFALKNGTITTTTPVKTNFGYHVILKENSQAKGQIKFDEVKQGIENGLKFEEFK 254

Query: 280 ERMNQRIEELRKHAKI 295  
+ +NQ+ ++L AK+  
Sbjct: 255 KVINQKGQDLLNSAKV 270

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# UniProtKB/Swiss-Prot entry Q9ZK19

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## Entry information

Entry name	<b>EFTU_HELPJ</b>	
Primary accession number	<b>Q9ZK19</b>	
Secondary accession numbers	None	
Entered in Swiss-Prot in	Release 39, May 2000	
Sequence was last modified in	Release 39, May 2000	
Annotations were last modified in	Release 47, May 2005	
Name and origin of the protein		
Protein name	<b>Elongation factor Tu</b>	
Synonym	<b>EF-Tu</b>	
Gene name	<b>Name: tuf</b> <b>Synonyms: tufA</b> <b>OrderedLocusNames: JHP1128</b>	
From	Helicobacter pylori J99 (Campylobacter pylori J99)	[TaxID: 85963]
Taxonomy	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales; Helicobacteraceae; Helicobacter.	

## References

- [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 DOI=10.1038/16495; PubMed=9923682 [NCBI, ExPASy, EBI, Israel, Japan]  
 Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Trust T.J.;  
 "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."  
 Nature 397:176-180(1999).

## Comments

- **FUNCTION:** This protein promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis.
- **SUBUNIT:** Monomer (*By similarity*).
- **SUBCELLULAR LOCATION:** Cytoplasmic.
- **SIMILARITY:** Belongs to the GTP-binding elongation factor family. EF-Tu/EF-1A subfamily.

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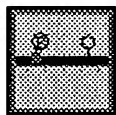
### Cross-references

EMBL	AE001541; AAD06711.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	E71844; E71844.	
HSSP	P02990; 1ETU. [HSSP ENTRY / PDB]	
SMR	Q9ZK19; 5-399.	
CMR	Q9ZK19; JHP1128.	
HAMAP	MF_00118; -; 1. PBIL [Family / Alignment / Tree]	
InterPro	IPR004541; EF-Tu. IPR004160; EFTU_Cterm. IPR004161; EFTU_D2. IPR000795; ProtSyn_GTPbind. IPR005225; Small_GTP. Graphical view of domain structure.	
Pfam	PF00009; GTP_EFTU; 1. PF03144; GTP_EFTU_D2; 1. PF03143; GTP_EFTU_D3; 1. Pfam graphical view of domain structure.	
PRINTS	PR00315; ELONGATNFCT.	
TIGRFAMs	TIGR00485; EF-Tu; 1. TIGR00231; small_GTP; 1.	
PROSITE	PS00301; EFACTOR_GTP; 1.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOGONOM	[Family / Alignment / Tree]	
BLOCKS	Q9ZK19.	
ProtoNet	Q9ZK19.	
ProtoMap	Q9ZK19.	
PRESAGE	Q9ZK19.	
DIP	Q9ZK19.	
ModBase	Q9ZK19.	
SWISS-2DPAGE	Get region on 2D PAGE.	
UniRef	View cluster of proteins with at least 50% / 90% identity.	

### Keywords

**Complete proteome; Elongation factor; GTP-binding; Protein biosynthesis.**

### Features



Feature table viewer

Key	From	To	Length	Description
NP_BIND	19	26	8	GTP (By similarity).
NP_BIND	81	85	5	GTP (By similarity).
NP_BIND	136	139	4	GTP (By similarity).

## Sequence information

Length: 399 Molecular weight: 43730 CRC64: 4E72A877BFCD104B [This is a checksum on the AA Da sequence]

```

      10      20      30      40      50      60
MAKEKFNRTN PHVNIGTIGH VYHGKTTLSA AISAVLSLKG LAEMKDYDNI DNAPQEKERG

      70      80      90     100     110     120
ITIATSHIEY ETETRHYAHV DCPGHADYVK NMITGAAQMD GAILVVSAAAD GPMPQTREHI

     130     140     150     160     170     180
LLSRQVGVPVH IVVFLNKQDM VDDQELLELV EMEVRELLSA YEFPGDDTPI VAGSALRALE

     190     200     210     220     230     240
EAKAGNVGEW GEKVLKLMAE VDSYIPTPER DTEKTFLMPV EDVFSIAGRG TVVTGRIERG

     250     260     270     280     290     300
VVKVGDEVEI VGIRATQKTT VTGVEMFRKE LEKGEAGDNV GVLLRGTKKE EVERGMVLCK

     310     320     330     340     350     360
PGSITPHKKF EEEIYVLSKE EGGRHTPFFT NYRPQFYVRT TDVTGSITLP EGVEMVMMPGD

     370     380     390
NVKITVELIS PVALELGTKF AIREGGRTVG AGVVSNIIE

```

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format

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ExPASy/SIB  
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,  
Compute pI/Mw, PeptideMass, PeptideCutter,  
Dotlet (Java)



ScanProsite, MotifScan



Submit a homology modeling request to SWISS-  
MODEL



NPSA Sequence analysis  
tools



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If your question is not covered, please contact [<helpdesk@expasy.org>](mailto:helpdesk@expasy.org).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: 399 AA (of which 5% low-complexity regions filtered out)

Date run: 2005-06-08 05:58:30 UTC+0100 on sib-gml.unil.ch

Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]

Database: EXPASY/UniProtKB

1,974,938 sequences; 640,866,274 total letters

UniProt Release 5.1 consists of: Swiss-Prot Release 47.1 of 24-May-2005: 181821 en

TrEMBL Release 30.1 of 24-May-2005: 1748002 entrie

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#### List of potentially matching sequences

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Db	AC	Description	Score	E-value
<input checked="" type="checkbox"/>	sp	<a href="#">Q9ZK19</a> EFTU_HELPJ Elongation factor Tu (EF-Tu) [tuf] [Helicob...	<a href="#">743</a>	0.0
<input checked="" type="checkbox"/>	sp	<a href="#">P56003</a> EFTU_HELPY Elongation factor Tu (EF-Tu) [tuf] [Helicob...	<a href="#">728</a>	0.0
<input type="checkbox"/>	tr	<a href="#">Q7VJ74</a> _HELHP Translation elongation factor EF-Tu (EC 3.6.1.48...	<a href="#">680</a>	0.0
<input checked="" type="checkbox"/>	sp	<a href="#">P42482</a> EFTU_WOLSU Elongation factor Tu (EF-Tu) [tuf] [Wolinel...	<a href="#">667</a>	0.0
<input checked="" type="checkbox"/>	sp	<a href="#">Q69303</a> EFTU_CAMJE Elongation factor Tu (EF-Tu) [tuf] [Campylo...	<a href="#">637</a>	0.0
<input checked="" type="checkbox"/>	tr	<a href="#">Q5HVZ7</a> _CAMJR Translation elongation factor Tu [tuf] [Campylob...	<a href="#">637</a>	0.0
<input checked="" type="checkbox"/>	sp	<a href="#">P64027</a> EFTU_NEIMB Elongation factor Tu (EF-Tu) [tufA] [Neisse...	<a href="#">578</a>	e-164
<input checked="" type="checkbox"/>	sp	<a href="#">P64026</a> EFTU_NEIMA Elongation factor Tu (EF-Tu) [tufA] [Neisse...	<a href="#">578</a>	e-164
<input type="checkbox"/>	tr	<a href="#">Q748X8</a> _GEOSL Translation elongation factor Tu [tuf-2] [Geobac...	<a href="#">575</a>	e-163
<input type="checkbox"/>	tr	<a href="#">Q5F5Q8</a> _NEIG1 Translation elongation factor TU [NGO1842] [Neis...	<a href="#">575</a>	e-163

<input type="checkbox"/>	tr	<a href="#">Q839G8</a>	_ENTFA Translation elongation factor Tu [tuf] [Enteroco...	<a href="#">575</a>	e-163
<input type="checkbox"/>	tr	<a href="#">Q5NID9</a>	_FRATT Elongation factor Tu (EF-Tu) [tufA] [Francisella...	<a href="#">574</a>	e-162
<input type="checkbox"/>	sp	<a href="#">Q8XGZ0</a>	EFTU_RALSO Elongation factor Tu (EF-Tu) [tufA] [Ralsto...	<a href="#">573</a>	e-162
<input type="checkbox"/>	tr	<a href="#">Q7M7F1</a>	_CHRVO Translation elongation factor Tu (EC 3.6.1.48) [...]	<a href="#">573</a>	e-162
<input checked="" type="checkbox"/>	sp	<a href="#">Q50306</a>	EFTU_BACST Elongation factor Tu (EF-Tu) [tuf] [Bacillu...	<a href="#">571</a>	e-162
<input type="checkbox"/>	tr	<a href="#">Q5L3Z9</a>	_GEOKA Translation elongation factor Tu (EF-Tu) [tufA] ...	<a href="#">570</a>	e-161
<input type="checkbox"/>	tr	<a href="#">Q5P334</a>	_AZOSE Elongation factor Tu [tufB] [Azoarcus sp. (strai...	<a href="#">569</a>	e-161
<input type="checkbox"/>	sp	<a href="#">Q8R7T8</a>	EFTU2_THETN Elongation factor Tu-B (EF-Tu-B) [tufB] [T...	<a href="#">568</a>	e-161
<input type="checkbox"/>	sp	<a href="#">Q8R603</a>	EFTU_FUSNN Elongation factor Tu (EF-Tu) [tuf] [Fusobac...	<a href="#">568</a>	e-160
<input type="checkbox"/>	tr	<a href="#">Q63PZ6</a>	_BURPS Elongation factor Tu [tufA1] [Burkholderia pseud...	<a href="#">568</a>	e-160
<input type="checkbox"/>	tr	<a href="#">Q62GK3</a>	_BURMA Translation elongation factor Tu [tuf-1] [Burkho...	<a href="#">568</a>	e-160
<input type="checkbox"/>	sp	<a href="#">P42481</a>	EFTU_THICU Elongation factor Tu (EF-Tu) [tuf] [Thiobac...	<a href="#">567</a>	e-160
<input type="checkbox"/>	sp	<a href="#">P48864</a>	EFTU_NEIGO Elongation factor Tu (EF-Tu) [tuf] [Neisser...	<a href="#">567</a>	e-160
<input type="checkbox"/>	sp	<a href="#">Q8R7V2</a>	EFTU1_THETN Elongation factor Tu-A (EF-Tu-A) [tufA] [T...	<a href="#">567</a>	e-160
<input type="checkbox"/>	tr	<a href="#">Q83ES6</a>	_COXBU Translation elongation factor Tu [tuf-2] [Coxiel...	<a href="#">567</a>	e-160
<input type="checkbox"/>	tr	<a href="#">Q7P364</a>	_FUSNV Protein translation elongation factor Tu (EF-TU)...	<a href="#">567</a>	e-160
<input type="checkbox"/>	tr	<a href="#">Q7TTF9</a>	_HAEDU Elongation factor tu, EF-Tu [tufA] [Haemophilus ...]	<a href="#">567</a>	e-160
<input type="checkbox"/>	sp	<a href="#">Q99QM0</a>	EFTU_CAUCR Elongation factor Tu (EF-Tu) [tufA] [Caulob...	<a href="#">566</a>	e-160
<input type="checkbox"/>	sp	<a href="#">Q8Y422</a>	EFTU_LISMO Elongation factor Tu (EF-Tu) [tuf] [Listeri...	<a href="#">566</a>	e-160
<input type="checkbox"/>	sp	<a href="#">Q71WB9</a>	EFTU_LISMF Elongation factor Tu (EF-Tu) [tuf] [Listeri...	<a href="#">566</a>	e-160
<input type="checkbox"/>	sp	<a href="#">Q927I6</a>	EFTU_LISIN Elongation factor Tu (EF-Tu) [tuf] [Listeri...	<a href="#">566</a>	e-160
<input type="checkbox"/>	tr	<a href="#">Q81ZS3</a>	_NITEU GTPases-translation elongation factors and sulfa...	<a href="#">565</a>	e-160
<input type="checkbox"/>	sp	<a href="#">P57939</a>	EFTU1_PASMU Elongation factor Tu-A (EF-Tu-A) [tufA] [P...	<a href="#">565</a>	e-160
<input type="checkbox"/>	tr	<a href="#">Q65QG6</a>	_MANSM TufB protein [tufB] [Mannheimia succiniciproduce...	<a href="#">565</a>	e-160
<input type="checkbox"/>	tr	<a href="#">Q8L160</a>	_MYXXA Elongation factor Tu [tufA] [Myxococcus xanthus]	<a href="#">565</a>	e-160
<input type="checkbox"/>	tr	<a href="#">Q5FTY1</a>	_GLUOX Protein Translation Elongation Factor Tu (EF-TU)...	<a href="#">564</a>	e-159
<input type="checkbox"/>	sp	<a href="#">Q8ETY4</a>	EFTU_OCEIH Elongation factor Tu (EF-Tu) [tuf] [Oceanob...	<a href="#">564</a>	e-159
<input type="checkbox"/>	tr	<a href="#">Q605B0</a>	_METCA Translation elongation factor Tu [tuf-2] [Methyl...	<a href="#">563</a>	e-159
<input type="checkbox"/>	tr	<a href="#">Q8EK70</a>	_SHEON Translation elongation factor Tu [tufA] [Shewane...	<a href="#">563</a>	e-159
<input type="checkbox"/>	tr	<a href="#">Q7TT91</a>	_BORPE Elongation factor Tu [tufA] [Bordetella pertussis]	<a href="#">563</a>	e-159
<input type="checkbox"/>	tr	<a href="#">Q79GC6</a>	_BORPA Elongation factor Tu [tuf] [Bordetella parapertu...	<a href="#">563</a>	e-159
<input type="checkbox"/>	tr	<a href="#">Q79G84</a>	_BORBR Elongation factor Tu [tuf] [Bordetella bronchise...	<a href="#">563</a>	e-159
<input type="checkbox"/>	tr	<a href="#">Q5GWR8</a>	_XANOR Elongation factor Tu [tufB] [Xanthomonas oryzae ...]	<a href="#">563</a>	e-159
<input type="checkbox"/>	sp	<a href="#">P43926</a>	EFTU_HAEIN Elongation factor Tu (EF-Tu) [tufA] [Haemop...	<a href="#">562</a>	e-159
<input type="checkbox"/>	sp	<a href="#">P57966</a>	EFTU2_PASMU Elongation factor Tu-B (EF-Tu-B) [tufB] [P...	<a href="#">561</a>	e-159
<input type="checkbox"/>	tr	<a href="#">Q65PA9</a>	_BACLD TufA (Elongation factor Tu) [tufA] [Bacillus lic...	<a href="#">561</a>	e-159
<input type="checkbox"/>	sp	<a href="#">P33169</a>	EFTU_SHEPU Elongation factor Tu (EF-Tu) [tuf] [Shewane...	<a href="#">561</a>	e-158
<input type="checkbox"/>	tr	<a href="#">Q8EK81</a>	_SHEON Translation elongation factor Tu [tufB] [Shewane...	<a href="#">561</a>	e-158
<input type="checkbox"/>	tr	<a href="#">Q5NQ65</a>	_ZYMOM Translation elongation factor [ZMO0516] [Zymomon...	<a href="#">561</a>	e-158
<input type="checkbox"/>	sp	<a href="#">Q8CQ81</a>	EFTU_STAEP Elongation factor Tu (EF-Tu) [tuf] [Staphyl...	<a href="#">560</a>	e-158
<input type="checkbox"/>	sp	<a href="#">P33167</a>	EFTU_BURCE Elongation factor Tu (EF-Tu) [tuf] [Burkhol...	<a href="#">560</a>	e-158
<input type="checkbox"/>	tr	<a href="#">Q5HRK4</a>	_STAEQ Translation elongation factor Tu [tuf] [Staphylo...	<a href="#">560</a>	e-158
<input type="checkbox"/>	sp	<a href="#">Q929L6</a>	EFTU_BACHD Elongation factor Tu (EF-Tu) [tuf] [Bacillu...	<a href="#">560</a>	e-158
<input type="checkbox"/>	sp	<a href="#">Q8NL22</a>	EFTU_XANAC Elongation factor Tu (EF-Tu) [tufA] [Xantho...	<a href="#">560</a>	e-158
<input type="checkbox"/>	sp	<a href="#">P33166</a>	EFTU_BACSU Elongation factor Tu (EF-Tu) (P-40) [tuf] [...]	<a href="#">560</a>	e-158



<input type="checkbox"/>	sp	<a href="#">P64029</a>	EFTU_STAAB	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...	<a href="#">559</a>	e-158
<input type="checkbox"/>	sp	<a href="#">Q6GBT9</a>	EFTU_STAAS	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...	<a href="#">559</a>	e-158
<input type="checkbox"/>	sp	<a href="#">Q6GJC0</a>	EFTU_STAAR	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...	<a href="#">559</a>	e-158
<input type="checkbox"/>	sp	<a href="#">P99152</a>	EFTU_STAAN	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...	<a href="#">559</a>	e-158
<input type="checkbox"/>	sp	<a href="#">P64028</a>	EFTU_STAAM	Elongation factor Tu (EF-Tu)	[tuf]	[Staphyl...	<a href="#">559</a>	e-158
<input type="checkbox"/>	tr	<a href="#">Q5HIC7</a>	_STAAC	Translation elongation factor Tu	[tuf]	[Staphylo...	<a href="#">559</a>	e-158
<input type="checkbox"/>	tr	<a href="#">Q5QWA3</a>	_IDILO	Translation elongation factor EF-Tu	[tufB_1]	[Id...	<a href="#">559</a>	e-158
<input type="checkbox"/>	tr	<a href="#">Q6N4Q4</a>	_RHOPA	Elongation factor Tu (EC 3.6.1.48)	[tuf/ EF-Tu]	...	<a href="#">558</a>	e-158
<input type="checkbox"/>	tr	<a href="#">Q73F98</a>	_BACC1	Translation elongation factor Tu	[tuf]	[Bacillus...	<a href="#">558</a>	e-158
<input type="checkbox"/>	sp	<a href="#">Q814C4</a>	EFTU_BACCR	Elongation factor Tu (EF-Tu)	[tuf]	[Bacillu...	<a href="#">558</a>	e-158
<input type="checkbox"/>	sp	<a href="#">Q81VT2</a>	EFTU_BACAN	Elongation factor Tu (EF-Tu)	[tuf]	[Bacillu...	<a href="#">558</a>	e-158
<input type="checkbox"/>	tr	<a href="#">Q6HPR0</a>	_BACHK	Protein-synthesizing GTPase (Translation elongat...			<a href="#">558</a>	e-158
<input type="checkbox"/>	tr	<a href="#">Q63H92</a>	_BACCZ	Protein-synthesizing GTPase (Translation elongat...			<a href="#">558</a>	e-158
<input type="checkbox"/>	tr	<a href="#">Q6MJ00</a>	_BDEBA	Translation elongation factor Tu (EC 3.6.1.48)	[...]		<a href="#">557</a>	e-157
<input type="checkbox"/>	tr	<a href="#">Q9F9S8</a>	_9PROT	Eftu [eftu] [EDTA-degrading bacterium BNC1]			<a href="#">557</a>	e-157
<input type="checkbox"/>	tr	<a href="#">Q5PIW4</a>	_SALPA	Elongation factor Tu [tufA] [Salmonella paratyph...			<a href="#">556</a>	e-157
<input type="checkbox"/>	tr	<a href="#">Q57H76</a>	_SALCH	Protein chain elongation factor EF-Tu (Duplicate...			<a href="#">556</a>	e-157
<input type="checkbox"/>	tr	<a href="#">Q6N0C2</a>	_9PROT	EF-Tu [orf3309] [Magnetospirillum gryphiswaldense]			<a href="#">556</a>	e-157
<input type="checkbox"/>	sp	<a href="#">P26184</a>	EFTU_FLESI	Elongation factor Tu (EF-Tu)	[tuf]	[Flexist...	<a href="#">556</a>	e-157
<input type="checkbox"/>	sp	<a href="#">Q83JC4</a>	EFTU_SHIFL	Elongation factor Tu (EF-Tu)	[tufA]	[Shigel...	<a href="#">555</a>	e-157
<input type="checkbox"/>	sp	<a href="#">P0A6N1</a>	EFTU_ECOLI	Elongation factor Tu (EF-Tu) (P-43)	[tufA]	...	<a href="#">555</a>	e-157
<input type="checkbox"/>	sp	<a href="#">P0A6N2</a>	EFTU_ECOL6	Elongation factor Tu (EF-Tu) (P-43)	[tufA]	...	<a href="#">555</a>	e-157
<input type="checkbox"/>	sp	<a href="#">P0A6N3</a>	EFTU_ECO57	Elongation factor Tu (EF-Tu) (P-43)	[tufA]	...	<a href="#">555</a>	e-157
<input type="checkbox"/>	tr	<a href="#">Q5ZYP5</a>	_LEGPH	Translation elongation factor Tu (EF-Tu) (EC 3.6...			<a href="#">555</a>	e-157
<input type="checkbox"/>	tr	<a href="#">Q5X873</a>	_LEGPA	Translation elongation factor Tu [tufA] [Legione...			<a href="#">555</a>	e-157
<input type="checkbox"/>	tr	<a href="#">Q57J27</a>	_SALCH	Protein chain elongation factor EF-Tu (Duplicate...			<a href="#">555</a>	e-157
<input type="checkbox"/>	sp	<a href="#">P0A1H5</a>	EFTU_SALTY	Elongation factor Tu (EF-Tu)	[tufA]	[Salmon...	<a href="#">555</a>	e-157
<input type="checkbox"/>	sp	<a href="#">P0A1H6</a>	EFTU_SALTI	Elongation factor Tu (EF-Tu)	[tufA]	[Salmon...	<a href="#">555</a>	e-157
<input type="checkbox"/>	sp	<a href="#">O31298</a>	EFTU_BUCAP	Elongation factor Tu (EF-Tu)	[tuf]	[Buchner...	<a href="#">555</a>	e-157
<input type="checkbox"/>	tr	<a href="#">Q6FZC0</a>	_BARQU	Elongation factor tu (EF-tu)	[tuf1]	[Bartonella ...]	<a href="#">555</a>	e-157
<input type="checkbox"/>	tr	<a href="#">Q5WZL4</a>	_LEGPL	Elongation factor Tu [tufA] [Legionella pneumoph...			<a href="#">555</a>	e-157
<input type="checkbox"/>	sp	<a href="#">Q925Y6</a>	EFTU_RHIME	Elongation factor Tu (EF-Tu)	[tufA]	[Rhizob...	<a href="#">554</a>	e-156
<input type="checkbox"/>	tr	<a href="#">Q6FZL2</a>	_BARQU	Elongation factor tu (EF-tu)	[tuf2]	[Bartonella ...]	<a href="#">554</a>	e-156
<input type="checkbox"/>	tr	<a href="#">Q7MYE8</a>	_PHOLL	Elongation factor Tu (EF-Tu)	[tufA]	[Photorhabdu...	<a href="#">554</a>	e-156
<input type="checkbox"/>	sp	<a href="#">P18668</a>	EFTU_SYNP6	Elongation factor Tu (EF-Tu)	[tuf]	[Synecho...	<a href="#">554</a>	e-156
<input type="checkbox"/>	sp	<a href="#">O31297</a>	EFTU_BUCAI	Elongation factor Tu (EF-Tu)	[tuf]	[Buchner...	<a href="#">554</a>	e-156
<input type="checkbox"/>	sp	<a href="#">P33165</a>	EFTU_BACFR	Elongation factor Tu (EF-Tu)	[tuf]	[Bactero...	<a href="#">553</a>	e-156
<input type="checkbox"/>	sp	<a href="#">P33171</a>	EFTU_SYNP7	Elongation factor Tu (EF-Tu)	[tuf]	[Synecho...	<a href="#">553</a>	e-156
<input type="checkbox"/>	sp	<a href="#">Q8ZAN8</a>	EFTU2_YERPE	Elongation factor Tu-B (EF-Tu-B)	[tufB]	[Y...	<a href="#">553</a>	e-156
<input type="checkbox"/>	tr	<a href="#">Q66FQ9</a>	_YERPS	Elongation factor Tu [tufA] [Yersinia pseudotube...			<a href="#">553</a>	e-156
<input type="checkbox"/>	tr	<a href="#">Q8KHX9</a>	_BARHE	Elongation factor TU (EF-Tu)	[tufB]	[Bartonella ...]	<a href="#">552</a>	e-156
<input type="checkbox"/>	tr	<a href="#">Q89J82</a>	_BRAJA	Elongation factor TU [tuf]		[Bradyrhizobium japon...	<a href="#">552</a>	e-156
<input type="checkbox"/>	tr	<a href="#">Q727D5</a>	_DESVH	Translation elongation factor Tu [tuf]		[Desulfov...	<a href="#">552</a>	e-156
<input type="checkbox"/>	tr	<a href="#">Q7N9B1</a>	_PHOLL	Translation elongation factor EF-Tu.B	[tufB]	[Ph...	<a href="#">552</a>	e-156
<input type="checkbox"/>	sp	<a href="#">Q8UE16</a>	EFTU_AGRT5	Elongation factor Tu (EF-Tu)	[tufA]	[Agroba...	<a href="#">551</a>	e-156

## Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs  
( [Help](#)) (use [ScanProsite](#) for more details about PROSITE matches)

## Profile hits

## Pfam hits

GTP\_EFTU

GTP\_EFTU\_D2

GTP\_EFTU\_D3

Submission	Matches on query sequence		Mat
	1	50 100 150 200 250 300 350	
EFTU_HELPJ			
EFTU_HELPY			
Q7VJ74			
EFTU_HOLSU			
EFTU_CAMJE			
Q5HVZ7			
EFTU_NEIMB			
EFTU_NEIMA			
Q748X8			
Q5F5Q8			
Q839G8			
Q5NI09			
EFTU_RALSO			
Q7M7F1			
EFTU_BACST			
Q5L3Z9			
Q5P334			
EFTU2_THETH			
EFTU_FUSNN			
Q63PZ6			
Q62GK3			
EFTU_THICU			
EFTU_NEIGO			
EFTU1_THETH			
Q83ES6			
Q7P364			
Q7TTF9			
EFTU_CAUCR			
EFTU_LISM0			
EFTU_LISMF			
EFTU_LISIN			
Q81Z53			
EFTU1_PASHU			
Q65QG6			
Q8L160			
Q5FTY1			
EFTU_OCEIH			
Q605B0			
Q8EK70			
Q7T191			
Q79GC6			
Q79G84			
Q5GHR8			
EFTU_HAEIN			
EFTU2_PASHU			
Q65PA9			
EFTU_SHEPU			
Q8EK81			
Q5NQ65			
EFTU_STAEP			
EFTU_BURCE			
Q5HRK4			
EFTU_BACHD			
EFTU_XANAC			
EFTU_BACSU			
EFTU_STAAR			
EFTU_STAAS			
EFTU_STAAR			
EFTU_STAAR			
EFTU_STAAR			
Q5HIC7			
Q5QMA3			
Q6N4Q4			
Q73F98			
EFTU_BACCR			
EFTU_BACAN			
Q6HPR0			
Q63H92			
Q6MJ00			
Q9F9S8			
Q5PI44			
Q57H76			
Q6N0C2			
EFTU_FLESI			
EFTU_SHIFL			
EFTU_EC0L1			
EFTU_EC0L6			
EFTU_EC057			
Q5ZYP5			
Q5X873			
Q57J27			
EFTU_SALTY			
EFTU_SALTI			
EFTU_BUCAP			
Q6FZC0			
Q5HZL4			

## Alignments

sp Q9ZK19 Elongation factor Tu (EF-Tu) [tuf] [Helicobacter pylori] 399  
 EFTU\_HELPJ J99 AA  
 (Campylobacter pylori J99)] align

Score = 743 bits (1919), Expect = 0.0  
 Identities = 378/399 (94%), Positives = 378/399 (94%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG  
 Sbjct: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI  
 Sbjct: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVPPIVFLNK SAYEFPGDDTPIVAGSALRALE  
 Sbjct: 121 LLSRQVGVPPIVFLNKQDMVDDQELLELVEMEVRELLSAYEFPGDDTPIVAGSALRALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240  
 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG  
 Sbjct: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK  
 Sbjct: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360  
 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD  
 Sbjct: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE  
 Sbjct: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

sp P56003 Elongation factor Tu (EF-Tu) [tuf] [Helicobacter pylori] 399 AA  
 EFTU\_HELPY (Campylobacter pylori)] align

Score = 728 bits (1880), Expect = 0.0  
 Identities = 371/399 (92%), Positives = 373/399 (92%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG  
 Sbjct: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI  
 Sbjct: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVPPIVFLNK SAYEFPGDDTPIVAGSALRALE

Sbjct: 121 LLSRQVGVP HIVVFLNKQDMVDDQELLELVEMEVRELLSAYEFPGDDTPIVAGSALRALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG 240  
EAKAGNVGEWGEKVLKLM AEVD+YIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG

Sbjct: 181 EAKAGNVGEWGEKVLKLM AEVDAYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
VVKVGDEVEIVGIR TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK

Sbjct: 241 VVKVGDEVEIVGIRPTQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360  
PGSITPHKKFE EIIYVLSKEEGGRHTPFFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD

Sbjct: 301 PGSITPHKKFEGEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE

Sbjct: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

tr Q7VJ74 Translation elongation factor EF-Tu (EC 3.6.1.48) [tufA] 399 AA  
Q7VJ74\_HELHP [Helicobacter hepaticus]

align

Score = 680 bits (1755), Expect = 0.0  
Identities = 341/399 (85%), Positives = 360/399 (89%)

Query: 1 MAKEKFNRTNPHVNI GTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
MAKEKF + PHVN+GTIGHV HGKTTLSAAISAVL+ KGLAE+KDYDNIDNAP+EKERG

Sbjct: 1 MAKEKFNRTNPHVNI GTIGHVYHGKTTLSAAISAVLATKGLAELKDYDNIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILLVSAADGMPQTREHI 120  
ITIATSHIEYETE RHYAHVDCPGHADVKNMITGAAQMDGAILLVSAADGMPQTREHI

Sbjct: 61 ITIATSHIEYETENRHYAHVDCPGHADVKNMITGAAQMDGAILLVSAADGMPQTREHI 120

Query: 121 LLSRQVGVP HIVVFLNKXXXXXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
LLSRQVGVP +IIVVFLNK S Y+FPGDDTPT+AGSAL+ALE

Sbjct: 121 LLSRQVGVP HIVVFLNKQDMVDDAEELLELVEMEVRELLSQYDFPGDDTPIIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG 240  
EAKAGNVGEWGEKVLKLM EVD YIPT+RDEKTFILMPVEDVFSIAGRGT VVTGR+ERG

Sbjct: 181 EAKAGNVGEWGEKVLKLM EVDKYIPTPQRDTEKTFILMPVEDVFSIAGRGT VVTGRVERG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
VV+VGDEVEIVGIR TQKTTVTGVEMFRKEL+KGEAGDNVG+LLRGTKKEEVERGMVLCK

Sbjct: 241 VVKVGDEVEIVGIRDTQKTTVTGVEMFRKELDKGEAGDNVGVLLRGTKKEEVERGMVLCK 300

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360  
PGSITPHKKFE EIIYVLSK+EGGRHTPFF YRPQFYVRTT DVTGSI LP GVEMVMPGD

Sbjct: 301 PGSITPHKKFEGEIIYVLSKDEGGGRHTPFFNGYRPQFYVRTT DVTGSIELPSGVEMVMPGD 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
NVKITVELI+PVALE GT+FAIREGGRTVG+GVV+ IIE

Sbjct: 361 NVKITVELIAPVALEDGTRFAIREGGRTVGSGVVTKIIE 399

sp P42482 Elongation factor Tu (EF-Tu) [tuf] [Wolinella  
EFTU\_WOLSU succinogenes]

399  
AA  
align

Score = 667 bits (1720), Expect = 0.0  
Identities = 337/397 (84%), Positives = 353/397 (88%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MAKEKF + PHVNIGTIGHV HGKTTLSAAISAVL+ KGL E+KDYD IDNAP+E+ERG
Sbjct: 1  MAKEKFNRTNPHVNIGTIGHVDHGKTTLSAAISAVLATKGLCELKDYDAIDNAPEERERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120
        ITIATSHIEYETE RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI
Sbjct: 61  ITIATSHIEYETENRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LLSRQVGVP+IVVFLNK S Y+FFGDDTPIVAGSAL+ALE
Sbjct: 121  LLSRQVGVPPIVFLNKEDMVDDAELLELVEMEIRELLSNYDFPGDDTPIVAGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
        EAK GNVGEWGEKVLKLM AEVD YIPTPERD +K FLMPVEDVFSIAGRGT VVTGRIERG
Sbjct: 181  EAKTGNVGEWGEKVLKLM AEVDRIYIPTPERDVDPFLMPVEDVFSIAGRGT VVTGRIERG 240

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        VVKVGDEVEIVGIR TQKTTVTGVMFRKEL+KGEAGDNVGVLLRGTKKE+VERGMVLCK
Sbjct: 241  VVKVGDEVEIVGIRNTQKTTVTGVMFRKELDKGEAGDNVGVLLRGTKKEDVERGMVLCK 300

Query: 301  PGSITPHKKFEEEEIVLSKEEGGRHTPFFTNYPQFYVRTT DVTGSITLPEGVEMVMPGD 360
        GSTPH FE E+VLSKEEGGRHTPEE YRPQFYVRTT DVTGSI+LPEGVEMVMPGD
Sbjct: 301  IGSITPHTNFEGEVVLSKEEGGRHTPFFNGYRPFYVRTT DVTGSISLPEGVEMVMPGD 360

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
        NVKI VELI+PVALE GP+FAIREGGRTVGAGVV+ I
Sbjct: 361  NVKINVELIAPVALEEGTRFAIREGGRTVGAGVVTKI 397

```

sp O69303 Elongation factor Tu (EF-Tu) [tuf] [Campylobacter jejuni] 399 AA  
EFTU\_CAMJE

align

Score = 637 bits (1644), Expect = 0.0  
Identities = 315/399 (78%), Positives = 350/399 (86%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MAKEKF+R PHVNIGTIGHV HGKTTLSAAISAVLS +GLAE+KDYDNIDNAP+EKERG
Sbjct: 1  MAKEKFSRNKPHVNIGTIGHVDHGKTTLTAAISAVLSRRGLAELKDYDNIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120
        ITIATSHIEYET+ RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI
Sbjct: 61  ITIATSHIEYETDNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LLSRQVGVP+IVVF+NK S+Y+FFGDDTPI++GSAL+ALE
Sbjct: 121  LLSRQVGVPPIVFMNKADMVDDAELLELVEMEIRELLSSYDFPGDDTPIISGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
        EAKAG GEW K++ LMA VDSYIPTP RDTEK FLMP+EDVFSI+GRGT VVTGRIE+G

```

Sbjct: 181 EAKAGQDGEWSAKIMDLMAAVDSYIPTPTRDTEKDFLMPIEDVFSISGRGTVVVTGRIEKG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
VVKVGD +EIVGI+ TQ TTVTGVEMFRKE+++GEAGDNVGVLLRGTKKEEV RGMVL K

Sbjct: 241 VVKVGDTIEIVGIKDTQTTTGTGVEMFRKEMDQGEAGDNVGVLLRGTKKEEVIRGMVLAK 300

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360  
P SITPH FE E+Y+L+K+EGGRHTPFF NYRPQFYVRTTDDVTGSI L +GVEMVMPG+

Sbjct: 301 PKSITPHTDFAEVIILNKDEGGGRHTPFFFNRYRPQFYVRTTDDVTGSIKLDGDEMMPGE 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
NV+ITV LI+PVALE GT+FAIREGG+TVG+GVVS II+

Sbjct: 361 NVRITVSLIAPVALEEGTRFAIREGGKTVGSGVVSIIK 399

tr Q5HVZ7 Translation elongation factor Tu [tuf] [Campylobacter] 399  
Q5HVZ7\_CAMJR jejuni AA  
(strain RM1221) align

Score = 637 bits (1644), Expect = 0.0  
Identities = 315/399 (78%), Positives = 350/399 (86%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
MAKEKF+R PHVNIGTIGHV HGKTTL+AAISAVLS +GLAE+KDYDNIDNAP+EKERG

Sbjct: 1 MAKEKFSRNKPHVNIGTIGHVDHGKTTLTAAISAVLSRRGLAELKDYDNIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQOTREHI 120  
ITIATSHIEYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQOTREHI

Sbjct: 61 ITIATSHIEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQOTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
LLSRQVGVP+IVVF+NK S+Y+FPGDDTPI++GSAL+ALE

Sbjct: 121 LLSRQVGVPPIVFMNKADMVDDAELELVEMEIRELLSSYDFPGDDTPIISGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVVTGRIERG 240  
EAKAG GEW K++ LMA VDSYIPTP RTEK FIMP+EDVFSI+GRGTVVVTGRIE+G

Sbjct: 181 EAKAGQDGEWSAKIMDLMAAVDSYIPTPTRDTEKDFLMPIEDVFSISGRGTVVVTGRIEKG 240

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
VVKVGD +EIVGI+ TQ TTVTGVEMFRKE+++GEAGDNVGVLLRGTKKEEV RGMVL K

Sbjct: 241 VVKVGDTIEIVGIKDTQTTTGTGVEMFRKEMDQGEAGDNVGVLLRGTKKEEVIRGMVLAK 300

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360  
P SITPH FE E+Y+L+K+EGGRHTPFF NYRPQFYVRTTDDVTGSI L +GVEMVMPG+

Sbjct: 301 PKSITPHTDFAEVIILNKDEGGGRHTPFFFNRYRPQFYVRTTDDVTGSIKLDGDEMMPGE 360

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
NV+ITV LI+PVALE GT+FAIREGG+TVG+GVVS II+

Sbjct: 361 NVRITVSLIAPVALEEGTRFAIREGGKTVGSGVVSIIK 399

sp P64027 Elongation factor Tu (EF-Tu) [tufA] [Neisseria] 394  
EFTU\_NEIMB meningitidis AA  
(serogroup B) align

Score = 578 bits (1490), Expect = e-164

Identities = 284/398 (71%), Positives = 331/398 (82%), Gaps = 5/398 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
        MAKEKF R+ PHVN+GTIGHV HGKTTL+AA++ +L+ K      K YD IDNAP+EK RG
Sbjct: 1  MAKEKFERSKPHVNVGTIGHVDHGKTTTLTAALTTLAKKFGGAAYDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
        ITI TSH+EYETETRHYAHVDCPGHADVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 61  ITINTSHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LL+RQVGVP+I+VF+NK                      S+Y+EPGDD PIV GSAL+ALE
Sbjct: 121  LLARQVGVPYIIIVFMNKCVMDDAELLELVEMEIRDLLSSYDFPGDDCPIVQGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
        A      + EK+ +L A +DSYIPTPER +K FL+P+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181  GDAA-----YEEKIFELAAALDSYIPTPERAVDKPFLLPIDVFSISGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300
        ++ VGDE+ELVG++ TQKTT TGVEMFRK L++G+AGDNVGVLLRGTKE+EVERG VL K
Sbjct: 236  IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLDEGQAGDNVGVLLRGTKEEDVERGQVLAK 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPPQFYVRTTDTVGSITLPEGVEMVMPGD 360
        PG+ITPH KP+ E+YVLSKEEGGRHTFFF NYRPPQFY RTTDTVGS++TL EGVEMVMPG+
Sbjct: 296  PGTITPHTKFAEVYVLSKEEGGRHTPFFFANYRPPQFYFRTTDTVGTAVTLEEGVEMVMPGE 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
        NV ITVELI+P+A+E G +FAIREGGRTVGAGVVS++I
Sbjct: 356  NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVVSNI 393

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sp P64026      Elongation factor Tu (EF-Tu) [tufA] [Neisseria      394
EFTU_NEIMA    meningitidis                                     AA
               (serogroup A)]                                  align

```

Score = 578 bits (1490), Expect = e-164

Identities = 284/398 (71%), Positives = 331/398 (82%), Gaps = 5/398 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
        MAKEKF R+ PHVN+GTIGHV HGKTTL+AA++ +L+ K      K YD IDNAP+EK RG
Sbjct: 1  MAKEKFERSKPHVNVGTIGHVDHGKTTTLTAALTTLAKKFGGAAYDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
        ITI TSH+EYETETRHYAHVDCPGHADVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 61  ITINTSHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LL+RQVGVP+I+VF+NK                      S+Y+EPGDD PIV GSAL+ALE
Sbjct: 121  LLARQVGVPYIIIVFMNKCVMDDAELLELVEMEIRDLLSSYDFPGDDCPIVQGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
        A      + EK+ +L A +DSYIPTPER +K FL+P+EDVEST+GRGTVVTGR+ERG
Sbjct: 181  GDAA-----YEEKIFELAAALDSYIPTPERAVDKPFLLPIDVFSISGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300

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      ++ VGDE+ELVG++ TQKTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VL K
Sbjct: 236 IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLDEGQAGDNVGVLLRGTKREDVERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
      PG+ITPH KF+ E+YVLSKEEGGRHTFFF NYRPQFY RTTDTG++TL EGVEMVMPG+
Sbjct: 296 PGTITPHTKFKAEVYVLSKEEGGRHTPFFANYRPQFYFRTTDTGAVTLEEGVEMVMPGE 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      NV ITVELI+P+A+E G +FAIREGGRTVGAGVVS++T
Sbjct: 356 NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVVSSVI 393

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tr Q748X8      Translation elongation factor Tu [tuf-2] [Geobacter      396
  Q748X8_GEOSL sulfurreducens] AA
                                         align

```

Score = 575 bits (1482), Expect = e-163  
 Identities = 285/400 (71%), Positives = 328/400 (81%), Gaps = 5/400 (1%)

```

Query: 1  MAKEKFNRNTNPVHNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK KF RT PHVNIQTIGHV HGKTTL+AAI+ VL+ +G AE + +D IDNAP+E+ERG
Sbjct: 1  MAKAKFERTKPHVHNIGTIGHVDHGKTTLTAAITKVLAERGQAEFRGFDQIDNAPEERERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITIATSH+EYETE RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 61  ITIATSHVEYETEKRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+IVVFLNK S+Y+FFGDD PI+ GSAL+ L
Sbjct: 121  LLARQVGVPYIVVFLNKADMVDDEELLELEIRELLSSYDFPGDDIPIIKGSALKGLN 180

Query: 181  EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVGTGRIER 239
      G+ E GE+ +LKLM VD+YIF PER +K FLMPVEDVFSI+GRGTV TGR+ER
Sbjct: 181  ----GDKDELGEEAILKLMEAVDNYIPEPERAVDKPFLMPVEDVFSISGRGTVATGRVER 236

Query: 240  GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      G+VKVG+EVEIVGI+AT KTTVTGVEMFRK L++G AGDN+G LLRG K+E++ERG VL
Sbjct: 237  GIVKVGEEVEIVGIKATAKTTVTGVEMFRKLLDEGRAGDNIGALLRGVKREDIERGQVLA 296

Query: 300  KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPG 359
      KPGSITPH KF+ E Y+L+KEEGGRHTFFF YRPQFY RTTDTG + LP G EMVMPG
Sbjct: 297  KPGSITPHTKFKAEAYILTKEEGGRHTPFFNGYRPQFYFRTTDTGVVDLPAGTEMVMPG 356

Query: 360  DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNV +T+ LI+P+A++ G +FAIREGGRTVGAGVVS+IIE
Sbjct: 357  DNVAVTINLITPIAMDEGLRFAIREGGRTVGAGVVSSIIE 396

```

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tr Q5F5Q8      Translation elongation factor TU [NGO1842] [Neisseria      394
  Q5F5Q8_NEIG1 gonorrhoeae
      (strain ATCC 700825 / FA 1090)] AA
                                         align

```

Score = 575 bits (1482), Expect = e-163  
 Identities = 282/398 (70%), Positives = 330/398 (82%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKF R+ PHVN+GTIGHV HGKTTL+AA++ +L+ K K YD IDNAP+EK RG  
 Sbjct: 1 MAKEKFSKPHVNVGTIGHVDHGKTTLTAALTILAKKFGGAAYDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI TSH+EYETETRHYAHVDCPGHADVKNMITGAAQMDGAILV SAADGMPQTREHI  
 Sbjct: 61 ITINTSHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP+I+VF+NK S+Y+FPGDD PIV GSAL+ALE  
 Sbjct: 121 LLARQVGVPYIIVFMNKCMDVDDAELLELVEMEIRDLLSSYDFPGDDCPVQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVTGRIERG 240  
 A + EK+ +L +DSYIPTER +K FL+P+EDVFSI+GRGTVVTGR+ERG  
 Sbjct: 181 GDAA-----YEEKIFELATALDSYIPTPERAVDKPFLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 ++ VGDE+EIVG++ TQKTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VL K  
 Sbjct: 236 IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLDEGQAGDNVGVLLRGTKREDVERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360  
 PG+ITPH KF+ E+YVLSKEEGGRHTPF FT NYRPQFY RTTDTVGT++TL +GVEMVMPG+  
 Sbjct: 296 PGTITPHTKFKAENVVLSKEEGGRHTPFFANYRPQFYFRTTDTVGTAVTLEKGVEMVMPGE 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398  
 NV ITVELI+P+A+E G +FAIREGGRTVGAGVVS++I  
 Sbjct: 356 NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVSSVI 393

tr Q839G8 Translation elongation factor Tu [tuf] [Enterococcus 395  
 Q839G8\_ENTFA faecalis AA  
 (Streptococcus faecalis)] align

Score = 575 bits (1481), Expect = e-163  
 Identities = 288/400 (72%), Positives = 328/400 (82%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKF+P+ HVNIGTIGHV HGKTTL+AAI+ VLS G E + YD+IDNAP+EKERG  
 Sbjct: 1 MAKEKFDRSKSHVNIGTIGHVDHGKTTLTAATVLSKHGGGEAQSYDSIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI TSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 61 ITINTSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LLSR VGVP+IVVFINK S Y+FPGDD P++AGSAL+ALE  
 Sbjct: 121 LLSRNVGVPIVFLNKMMDVDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVTGRIERG 240  
 ++ + EK+L+LMA VD YIPTPERD+K F+MPVEDVFSI GRGTV TGR+ERG  
 Sbjct: 181 GDES-----YEEKILELMAAVDEYIPTPERDTPKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIR-ATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 V+VGDEVEIVGI+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E++ERG VL  
 Sbjct: 236 EVRVGDEVEIVGIKDETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIERGQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPPQFYVRTTDVTGSITLPEGVEMVMPG 359  
 KP +ITPH KP+ E+YVLSKEEGGRHTPFFFTNYRPPQFY RYTDVTG + LPEG EMVMPG  
 Sbjct: 296 KPATITPHTKFKAEVYVLSKEEGGRHTPFFFTNYRPPQFYRRTTDVTGVVLEPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV + VELI P+A+E GT+F+IREGGRTVG+GVV+ I++  
 Sbjct: 356 DNVAMDVELIHPIAIEDGTRFSIREGGRTVGSGVVTEIVK 395

tr Q5NID9 Elongation factor Tu (EF-Tu) [tufA] [Francisella 394  
 Q5NID9\_FRATT tularensis (subsp. AA  
 tularensis)] align

Score = 574 bits (1480), Expect = e-162  
 Identities = 281/399 (70%); Positives = 328/399 (81%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKF R+ PHVN+GTIGHV HGKTTL+AAI+ V++ K + +D ID+AP+EK RG  
 Sbjct: 1 MAKEKFERSKPHVNVGTIGHVDHGKTTLTAAITKVMAEKNGGMARKFDEIDSAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI TSH+EYE+ RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI  
 Sbjct: 61 ITINTSHVEYESPNRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVP HIVVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP IVVFLNK YEFPGDDT++ GSALKA+E  
 Sbjct: 121 LLSRQVGVPKIVVFLNKCDMVDDEELLELVEMEVRELLDQYEFPGDDTPVIMGSALRAIE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240  
 +A + EK+++L+ +D YIP PERDTEK F++P+EDVESI+GRGTVVTGRIERG  
 Sbjct: 181 GDEA-----YVEKIVELVQAMDDYIPAPERDTEKPFILPIEDVFSISGRGTVVTGRIERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 VV +GDEVE+VGIR TQKTTVTGVEMFRK L++GEASDNVG+L+RG K+++VERG VLCK  
 Sbjct: 236 VVNIGDEVEVVGIRPTQKTTVTGVEMFRKLLDRGEAGDNVGVILVRGLKRDDVERGQVLCK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPPQFYVRTTDVTGSITLPEGVEMVMPGD 360  
 PGSI PH KFE E+YVLSKEEGGRHTPFF YRPPQFY RTTD+TG++ LPEGVEMVMPGD  
 Sbjct: 296 PGSIKPHTKFEAEVYVLSKEEGGRHTPFFKGYRPPQFYRRTTDITGAVELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NVK+T+ LI+P+A++ G +FAIREGGRTVGAGVV+ IIE  
 Sbjct: 356 NVKMTITLINPIAMDEGLRFAIREGGRTVGAGVVAKIIE 394

sp Q8XGZ0 Elongation factor Tu (EF-Tu) [tufA] [Ralstonia 396  
 EFTU\_RALSO solanacearum AA  
 (Pseudomonas solanacearum)] align

Score = 573 bits (1477), Expect = e-162  
 Identities = 289/400 (72%); Positives = 327/400 (81%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K E K YD ID AP+EK RG  
 Sbjct: 1 MAKEKFERTKPHVNVGTIGHVDHGKTTLTAAIATVLSKFGGEAKKYDEIDAAPEEKARG 60

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Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120
      ITI T+HIEYET RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 61 ITINTAHIEYETANRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+I+VFLNK S Y+FPGDDTPI+ GSA ALE
Sbjct: 121 LLARQVGVPYIIIVFLNKCDMVDDAELELVEMEVRELLSKYDFPGDDTPIIKGSAKLALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVGTGRIER 239
      G+ GE GE + +A+ +DSYIPTPER + TFLMPVEDVFSI+GRGTVVGTGRIER
Sbjct: 181 ----GDKGELGEVAIMNLADALDSYIPTPERAVDGTFLMPVEDVFSISGRGTVVGTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      G++KVG+E+EI VGI+ATQKTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VLC
Sbjct: 237 GIIKVGEEIEIVGIKATQKTTCTGVEMFRKLLDQGQAGDNVGILLRGTKREDVERGQVLC 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
      KPGSI PH F E+Y+LSK+EGGRHTFFF NYRPQFY RTTDTGSI LP+ EMVMPG
Sbjct: 297 KPGSIKPHHTFTGEVYILSKDEGGRHTPFFNNYRPQFYFRTTDTGSIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ IIE
Sbjct: 357 DNVSITVKLIAPIAMEEGLRFAIREGGRTVGAGVVAKIIE 396

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tr Q7M7F1 Translation elongation factor Tu (EC 3.6.1.48) [tufA] 396 AA  
 Q7M7F1\_CHRVO [Chromobacterium violaceum]  
 align

Score = 573 bits (1477), Expect = e-162

Identities = 286/399 (71%), Positives = 329/399 (81%), Gaps = 5/399 (1%)

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Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      MAKEKE RT PHVN+GTIGHV HGKTTL+AAI+ +LS K E KDY ID+AP+EK RG
Sbjct: 1 MAKEKFERTKPHVNVGTIGHVDHGKTTLTAAITILSKKFGGEAKDYSQIDSAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120
      ITI T+H+IEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 61 ITINTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+I+V+LNK S+Y+FPGDDTPIV GSA ALE
Sbjct: 121 LLSRQVGVPYIIIVYLNKADLVDDAELELVEMEVRLDLSYDFPGDDTPIVTGSARLALE 180

Query: 181 EAKAGNVGEWGE-KVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVGTGRIER 239
      G+ E GE + +L +DSYIPTPER +K FL+P+EDVFSI+GRGTVVGTGR+ER
Sbjct: 181 ----GDQSEMGEPSIFRLADALDSYIPTPERAIDKPFLLPIEDVFSISGRGTVVGTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      G+VKG+E+EI VGI+ T KTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VL
Sbjct: 237 GIVKVGEEIEIVGLKDTVKTCTGVEMFRKLLDQGQAGDNVGVLLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
      KPG+ITPH KFE +YVLSK+EGGRHTFFF NYRPQFY RTTDTG+I+L EGVEMVMPG
Sbjct: 297 KPGTITPHTKFEASVYVLSKDEGGRHTPFFFANYRPQFYFRTTDTGTAISLAEGVEMVMPG 356

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Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398  
 DNV+I VELL+P+A+E G +FAIREGGRTVGAGVV+ II  
 Sbjct: 357 DNVEIKVELIAPIAIMEEGLRFAIREGGRTVGAGVAKII 395

sp 050306 Elongation factor Tu (EF-Tu) [tuf] [Bacillus 395  
 EFTU\_BACST stearothermophilus] AA  
align

Score = 571 bits (1472), Expect = e-162  
 Identities = 283/400 (70%), Positives = 327/400 (81%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF RT PHVNIGTIGHV HGKTTL+AAI+ VL+ +G AE K YD ID AP+E+ERG  
 Sbjct: 1 MAKAKFERTKPHVNIGTIGHVDHGKTTLTAAITTVLAKQGKAEAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI+T+H+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 61 ITISTAHVEYETEARHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP+IVVFLNK S Y+FPGD+ P++ GSAL+ALE  
 Sbjct: 121 LLSRQVGVPYIVVFLNKCDMVDDEELLELVEMEVRDLLSEYDFPGDEVPVIKGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKILMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVTGRIERG 240  
 +W EK+++LM VD YITP+R+ +K F+MP+EDVFSI GRGTV TGR+ERG  
 Sbjct: 181 -----GDPKWEKIIELMNAVDEYIPTQREVDPKPFMPPIEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQK-TTVTGVMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 +KVGQ VEL+G+ K TTVTGVMFRK L++ EAGDN+G LRG ++EVERG VL  
 Sbjct: 236 TLKVGDPVEIIGLSDEPKATTVTGVEMFRKLLDQAEAGDNIGALLRGVSRDEVERGQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVTGSITLPEGVEMVMPG 359  
 KPGSITPH KF+ ++YVL+KEEGGRHTFFF+NYRPQFY RTTDTVTG ITLPEGVEMVMPG  
 Sbjct: 296 KPGSITPHTKFKAQVYVLTKEEGGRHTPFFSNYRPQFYFRTTDTVTGIITLPEGVEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV++TVELI+P+A+E GTKF+IREGGRTVGAG VS IIE  
 Sbjct: 356 DNVENTVELIAPIAIEEGTKFSIREGGRTVGAGSVSEIIE 395

tr Q5L3Z9 Translation elongation factor Tu (EF-Tu) [tufA] 395  
 Q5L3Z9\_GEOKA [Geobacillus  
 kaustophilus] AA  
align

Score = 570 bits (1470), Expect = e-161  
 Identities = 282/400 (70%), Positives = 327/400 (81%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF RT PHVNIGTIGHV HGKTTL+AAI+ VL+ +G AE K YD ID AP+E+ERG  
 Sbjct: 1 MAKAKFERTKPHVNIGTIGHVDHGKTTLTAAITTVLAKQGKAEAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI

Sbjct: 61 ITISTAHVEYETDARHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP+IVVFLNK S Y+FPGD+ P++ GSAL+ALE

Sbjct: 121 LLSRQVGVPPIVFLNKCDMVDDEELLELVEMEVRLDSEYDFPGDEVPVIKGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240  
 +W EK+++LM VD YIPTP+R+ +K F+MP+EDVFSI GRGTV TGR+ERG

Sbjct: 181 -----GDPQWEEKIIELMNAVDEYIPTPQREVDPKFMPIEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQK-TTGTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 +KVGQ VEL+G+ K TTGTGVEMFRK L++ EAGDN+G LLRG ++EVERG VL

Sbjct: 236 TLKVGDPVEIIGLSDEPKTTTGTGVEMFRKLLDQAEAGDNIGALLRGVSRDEVERGQVLA 295

Query: 300 KPGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPG 359  
 KPGSITPH KF+ ++YVL+KEEGGRHTPFF+NYRPQFY RTTDTG SIITLPEGVEMVMPG

Sbjct: 296 KPGSITPHTKFKAQVYVLTKEEGGRHTPFFSNYRPQFYFRTTDTGTIITLPEGVEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV++TVELI+P+A+E GTKF+IREGGRTVGAG VS IIE

Sbjct: 356 DNVEMTVELIAPIAIEEGTKFSIREGGRTVGAGSVSEIIE 395

tr Q5P334 Elongation factor Tu [tufB] [Azoarcus sp. (strain EbN1)] 396 AA  
 Q5P334\_AZOSE align

Score = 569 bits (1466), Expect = e-161  
 Identities = 286/400 (71%), Positives = 326/400 (81%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ +LS K E K YD ID AP+EK RG

Sbjct: 1 MAKGKFERTKPHVNVGTIGHVDHGKTTLTAAITLILSKKFGGEAKAYDQIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI T+H+EYET RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI

Sbjct: 61 ITINTAHVEYETANRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP+I+VFLNK S Y+FPGD+ PI+ GSAL+ALE

Sbjct: 121 LLARQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSKYDFPGDDVPIIKGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AE-VDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239  
 G+ +GE + +AE +DSYIPTPER ++ EL+P+EDVFSI+GRGTVVTGR+ER

Sbjct: 181 ----GDQSDIGEP AIFRLAEALDSYIPTPERAIDRPFLLPIDVFSISGRGTVVTGRVER 236

Query: 240 GVKVGDEVEIVGIRATQKTTGTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 G+VKVG+EVEIVGI+AT KTT TGVEMFRK L++G+AGDNVGVLLRGTK+E+VERG VLC

Sbjct: 237 GIVKVGEEVEIVGIKATVKTCTGVEMFRKLLDQGGAGDNVGVLLRGTKREDVERGQVLC 296

Query: 300 KPGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPG 359  
 KPGSI PH F E+YVLSKEEGGRHTPFF NYRPQFY RTTDTGSI LPEG EMVMPG

Sbjct: 297 KPGSIKPHTHFTGEVYVLSKEEGGRHTPFFNNYRPQFYFRTTDTGSIELPEGTEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV ITV+L++P+A+E G +FAIREGGRTVGAGV+ IIE

Sbjct: 357 DNVSITVKLMAPIAMEEGLRFAIREGGRTVGAGVVAKIIIE 396

sp Q8R7T8 Elongation factor Tu-B (EF-Tu-B) [tufB] 400  
 EFTU2\_THETN [Thermoanaerobacter 400  
 tengcongensis] align

Score = 568 bits (1464), Expect = e-161  
 Identities = 284/400 (71%), Positives = 323/400 (80%), Gaps = 1/400 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK+KF RT PHVN+GTIGHV HGKTTL+AAI+ +LS GLA+ K YD ID AP+EK RG  
 Sbjct: 1 MAKQKFERTKPHVNVGTIGHVDHGKTTTLTAAILLILSKAGLAQAKGYDEIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 61 ITINTTHVEYETAKRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP+IVVFLNK + YEFPGD+TPIV GSAL+ALE  
 Sbjct: 121 LLARQVGVPYIVVFLNKADMVDDPELIELVEMEVDRLLNQYEFPGDETPIVVGSALEKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKFLMPVEDVFSIAGRGTVVTGRIERG 240  
 +W K+ +LM VD YIPTPERD +K FLMPVEDVFSI GRGTV TGR+ERG  
 Sbjct: 181 CGCGKRECQWCGKIWELMDVVDEYIPTPERDIDKPFMPVEDVFSITGRGTVATGRVERG 240

Query: 241 VVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 VVKVGDEVEI+G+ ++KT VTGVEMFRK L++ +AGEN+GVLLRG +K+EVERG VL  
 Sbjct: 241 KVKVGDEVEIIGLTTESRKTVVTGVEMFRKTLDEAQAGDNIGVLLRGIQKDEVERGQVIA 300

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIPLPEGVEMVMPG 359  
 KPG+I PH KFE ++YVL+KEEGGRHTPEFF YRPQFY RTTDTGTG+I LPEGVEMVMPG  
 Sbjct: 301 KPGTIKPHTKFEAQVYVLTKEEGGRHTPFFNGYRPFYFRTTDTGTIQLPEGVEMVMPG 360

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 D+V + VELI+P+A+E G KFAIREGGRTVGAGVVS IIE  
 Sbjct: 361 DHVTLRVELITPIAMEEGLKFAIREGGRTVGAGVVSIIIE 400

sp Q8R603 Elongation factor Tu (EF-Tu) [tuf] [Fusobacterium 394  
 EFTU\_FUSNN nucleatum (subsp. 400  
 nucleatum)] align

Score = 568 bits (1463), Expect = e-160  
 Identities = 280/397 (70%), Positives = 324/397 (81%), Gaps = 5/397 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEK+ R+ PHVNIGTIGHV HGKTT +AAIS VLS KG A D+D ID AP+EKERG  
 Sbjct: 1 MAKEKYNRSKPHVNIGTIGHVDHGKTTTAAISKVLSKDWASKVDFDQIDAAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI T+HIEYETE RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 61 ITINTAHIEYETEKRYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180

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      LLSRQVGVP+IVV+LNK          + Y FPGDD P++ GS+L AL
Sbjct: 121 LLSRQVGVPYIVVYLNKSDMVEDEELLELVEMEVRELLTEYGFPGDDIPVIRGSSLGALN 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      +      +W EK+L+LM VD+YIETPER ++ FLMP+EDVF+I GRGTVVTGR+ERG
Sbjct: 181 GEE-----KWVEKILELMEAVDNYIPTPERAVDQPFILMPIEDVFTITGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      V+KVG+E+EI VGI+ T KTF TGVEMFRK L++G+AGDN+GVLLRGTKKEEVERG VL K
Sbjct: 236 VIKVGEEIEIVGIKPTTKTTCTGVEMFRKLLDQGGAGDNIGVLLRGTKKEEVERGQVLAK 295

Query: 301 PGSITPHKKFEEIEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPGD 360
      PGSI PH F+ E+YVL+K+EGGRHTPFFFT YRPQFY RTTD+TG++TLP+GVEMVMPGD
Sbjct: 296 PGSIHPHTNFKGEVYVLTKEGGGRHTPFFTGYRPQFYFRTTDTITGAVTLPDGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
      N+ +TVELI P+A+E G +FAIREGGRTV +GVVS I
Sbjct: 356 NITMTVELIHPIAMEQGLRFAIREGGRTVASGVVSEI 392

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tr Q63PZ6 Elongation factor Tu [tufA1] [Burkholderia pseudomallei] 396 AA  
 Q63PZ6\_BURPS (Pseudomonas pseudomallei)]

align

Score = 568 bits (1463), Expect = e-160  
 Identities = 287/400 (71%), Positives = 325/400 (80%), Gaps = 5/400 (1%)

```

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAKEKE RT PHVN+GTIGHV HCKTTL+AAI+ VLS K E K YD ID AP+EK RG
Sbjct: 1 MAKEKFERTKPHVNVGTIGHVDHGKTTTLTAAIATVLSAKFGGEAKKYDEIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120
      ITI T+HIEYET RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 61 ITINTAHIEYETANRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+I+VFLNK          S Y+FPGDDTPI+ GSA ALE
Sbjct: 121 LLARQVGVPYIIVFLNKCDMVDDAEELLELVEMEVRELLSKYDFPGDDTPIIKGSAKLAL 180

Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239
      G+ GE GE + +A+ +D+YIETPER + FLMPVEDVFSI+GRGTVVTGR+ER
Sbjct: 181 ----GDKGELGEVAIMNLADALDYIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      GV+KVG+E+EI VGI+AE KTF TGVEMFRK L++G+AGDNV+LLRGTK+E+VERG VL
Sbjct: 237 GVIKVGEEIEIVGIKATAKTTCTGVEMFRKLLDQGGAGDNVGIILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPG 359
      KPGSITPH F E+YVLSK+EGGRHTPFFFT NYRPQFY RTTDTGSI LP+ EMVMPG
Sbjct: 297 KPGSITPHTHFTAIEVYVLSKDEGGGRHTPFNNYRPQFYFRTTDTGSIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ IIE
Sbjct: 357 DNVSITVKLIAPAMEEGLRFAIREGGRTVGAGVVAKIIE 396

```



tr Q62GK3 Translation elongation factor Tu [tuf-1] [Burkholderia 396  
 Q62GK3\_BURMA mallei AA  
 (Pseudomonas mallei)] align

Score = 568 bits (1463), Expect = e-160  
 Identities = 287/400 (71%), Positives = 325/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAKEKF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K E K YD ID AP+EK RG  
 Sbjct: 1 MAKEKFERTKPHVNVGTIGHVDHGKTTLTAAIATVLSAKFGGEAKKYDEIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120  
 ITI T+HIEYET RHYAHVDCPGHADVKNMITGAAQMDGAILV SAADGMPMPQTREHI  
 Sbjct: 61 ITINTAHIEYETANRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGMPMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP+I+VFLNK S Y+FPGDPTPI+ GSA ALE  
 Sbjct: 121 LLARQVGVPYIIIVFLNKCDMVDDAELELVEMEVRELLSKYDFPGDDTPIIKGSAKLAL 180

Query: 181 EAKAGNVGEWGEKVLKLMAE-VDSYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTGRIER 239  
 G+ GE GE + +A+ +D+YIPTPER + FLMPVEDVFSI+GRGT VVTGR+ER  
 Sbjct: 181 ----GDKGELGEVAIMNLADALDTYIPTPERAVDGAFLMPVEDVFSISGRGT VVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 GV+KVG+E+EI VGI+AT KPT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL  
 Sbjct: 237 GVIKVGEEIEIVGIKATAKTTCTGVEMFRKLLDQGGAGDNV GILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPG 359  
 KPGSITPH F E+YVLSK+EGGRHTPEE NYRPQFY RTT DVTGSI LP+ EMVMPG  
 Sbjct: 297 KPGSITPHTHFTAEVYVLSKDEGGRHTPFFNNYRPQFYFRTT DVTGSIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ IIE  
 Sbjct: 357 DNVSITVKLIAPIAMEEGLRFAIREGGRTVGAGVVAKIIE 396

sp P42481 Elongation factor Tu (EF-Tu) [tuf] [Thiobacillus cuprinus] 396 AA  
 EFTU\_THICU align

Score = 567 bits (1462), Expect = e-160  
 Identities = 285/400 (71%), Positives = 324/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K E K YD ID AP+EK RG  
 Sbjct: 1 MAKSKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLSSKFGGEAKAYDQIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120  
 ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI  
 Sbjct: 61 ITINTAHVEYETANRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP+I+VFLNK S Y+FPGDPTPI+ GSA ALE  
 Sbjct: 121 LLARQVGVPYIIIVFLNKCDMVDDAELELVEMEVRELLSKYDFPGDDTPIIKGSAKLAL 180

Query: 181 EAKAGNVGEWGE-KVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTGRIER 239  
 G+ GE GE +LKL +D+YIPTPER + FLMPVEDVFSI+GRGT VVTGR+ER

Sbjct: 181 ----GDKGELGEGAILKLAEALDTYIPTPERAVDGAFLMPVEDVFSISGRGTVVTRGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
G++KVG+E+EVG++ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+EEVERG VLC

Sbjct: 237 GIIKVGEEIEIVGLKPTLKTCTGVEMFRKLLDQGGAGDNVGILLRGTKREEVERGQVLC 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYPQFYVRTTDDVTGSITLPEGVEMVMPG 359  
KPGSI PH F E+YVLSK+EGGRHTPFF NYRPQFY RTTDDVTG+I LP+ EMVMPG

Sbjct: 297 KPGSIKPHHTFAEVYVLSKDEGGGRHTPFFNNYPQFYFRTTDDVTGAIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ IIE

Sbjct: 357 DNVSITVKLIAPIAMEEGLRFAIREGGRTVGAGVVAKIIE 396

sp P48864 Elongation factor Tu (EF-Tu) [tuf] [Neisseria gonorrhoeae] 394 AA  
EFTU\_NEIGO

align

Score = 567 bits (1462), Expect = e-160

Identities = 280/398 (70%), Positives = 327/398 (81%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
MAKEKF R+ PHVN+GTIGHV NGKTTL+AA++ +L+ K K YD IDNAP+EK RG

Sbjct: 1 MAKEKFERSKPHVNVGTIGHVDHGKTTTLTAALTILAKKFGGAAYDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGPMPTREHI 120  
ITI TSH+EYETETRHYAHVDCPGHADVKNMITGAAQMDGAILV SAADGPMPTREHI

Sbjct: 61 ITINTSHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGPMPTREHI 120

Query: 121 LLSRQGVGVPHIVVFLNXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
LL+RQGVGV+I+VE+NK S+Y+FPGDD PIV GSAL+ALE

Sbjct: 121 LLARQGVGPYIIVFMNKCDDVDAELFQLVEMEIRDLLSSYDFPGDDCPIVQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240  
A + EK+ +L +D YIPTER +K FL+P+EDVFSI+GRGTVVTR+ERG

Sbjct: 181 GDAA-----YEEKIFELATALDRYIPTPERAVDKPFLLPIDVFSISGRGTVVTRGRVER 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
++ VGDE+ELVG++ TQKTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL K

Sbjct: 236 IIHVGDEIEIVGLKETQKTTCTGVEMFRKLLDEGQAGDNVGVLLRGTKREDVERGQVLAK 295

Query: 301 PGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYPQFYVRTTDDVTGSITLPEGVEMVMPGD 360  
G+ITPH KF+ E+YVLSKEEGG HTFFF NYRPQFY RTTDDVTG+ITL +GVEMVMPG+

Sbjct: 296 RGTITPHTKFAEVYVLSKEEGGPHTPFFANYRPQFYFRTTDDVTGTITLEKGVEMVMPGE 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 398  
NV ITVELI+P+A+E G +FAIREGGRTVGAGVVS+I

Sbjct: 356 NVTITVELIAPIAMEEGLRFAIREGGRTVGAGVVSNI 393

sp Q8R7V2 Elongation factor Tu-A (EF-Tu-A) [tufA]  
EFTU1\_THETN [Thermoanaerobacter  
tengcongensis]

400

AA

align

Score = 567 bits (1462), Expect = e-160

Identities = 283/400 (70%), Positives = 323/400 (80%), Gaps = 1/400 (0%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK+KF RT PHVN+GTIGHV HGKTTL+AAI+ +LS GLA+ K YD ID AP+EK RG
Sbjct: 1  MAKQKFERTKPHVNVGTIGHVDHGKTTLTAAITLILSKAGLAQAKGYDEIDKAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI T+H+EYET RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 61  ITINTTHVEYETAKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP+IVVFLNK + YEFPGDDTPIV GSAL+ALE
Sbjct: 121  LLARQVGVPYIVVFLNKADMVDDPELIELVEMEVRLDNLQYEFPGDDTPIVVSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
      +W K+ +LM VD YITPERD +K FIMPVEDVF+I GRGTV TGR+ERG
Sbjct: 181  CGCGKRECQWCGKIWELMDVDEYIPTPERDIDKPFMLPVEDVFTITGRGTVATGRVERG 240

Query: 241  VVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLC 299
      VVKVGDEVEL+G+ ++KT VTGVEMFRK L++ +AGDN+GVLLRG +++EVERG VL
Sbjct: 241  KVKVGDEVEIIGLTTESRKTVVTGVEMFRKTLDEAQAGDNIGVLLRGIQRDEVERGQVLA 300

Query: 300  KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVTSITLPEGVEMVMPG 359
      KPG+I PH KFE ++YVL+KEEGGRHTPFF YRPQFY RTTDTVTG+I LPEGVEMVMPG
Sbjct: 301  KPGTIKPHTKFEAQVYVLTKEEGGRHTPFFNGYRPQFYFRTTDTVTGTIQLPEGVEMVMPG 360

Query: 360  DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      D+V + VELI+P+A+E G KFAIREGGRTVGAGVVS IIE
Sbjct: 361  DHVTLRVELITPIAMEEGLKFAIREGGRTVGAGVVSNIIE 400

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tr Q83ES6      Translation elongation factor Tu [tuf-2] [Coxiella      397
   Q83ES6_COXBU burnetii]                                     AA
                                                           align

```

Score = 567 bits (1462), Expect = e-160

Identities = 281/400 (70%), Positives = 333/400 (83%), Gaps = 4/400 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      M+KEKF R PHVN+GTIGHV HGKTTL+AA++ VLS K E K +D IDNAP+E+ RG
Sbjct: 1  MSKEKFVREKPHVNVGTIGHVDHGKTTLTAAALTQVLSEKYGGEKKAFFDQIDNAPEERARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITIATSH+EY+++ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 61  ITIATSHVEYQSDKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      +L++QVGVP+IVV+LNK +Y+FFGD+TPT+ GSAL+ALE
Sbjct: 121  VLAKQVGVPNIVVYLNKADMVDDKELLELVEMEVRLDNLNSYDFPGDETPIIVGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
      K+ VGE ++KL+ +D+Y P ERK +K FLMP+EDVEST+GRGTVVTGR+ERG
Sbjct: 181  GDKS-EVGE--PSIIKLVTMDTYFPQPERAIDKPFMLPIEDVFSISGRGTVVTGRVERG 237

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300

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      ++KVGDE+ELVGI+ T KTF TGVEMFRK L++G+AGDNVG+LLRGTG+EEVERG VL K
Sbjct: 238 IIKVGDEIEIVGIKDTTKTTCTGVEMFRKLLDEGQAGDNVIGILLRGTGKREEVERGQVLAK 297

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGS-ITLPEGVEMVMPG 359
      PGSITPHKKFE ELYVLSKEEGGRHTPF YRPQFY RTTDTVGS ++LPEG+EMVMPG
Sbjct: 298 PGSITPHKKFEAEIYVLSKEEGGRHTPFLOGYRPOFYFRTTDTVGTQLLSLPEGIEMVMPG 357

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNVK+TVELI+EVA++ G +FA+REGGRTVGAGVV+ IIE
Sbjct: 358 DNVKVTVELIAPVAMDEGLRFAVREGGRTVGAGVVTKIIE 397

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tr Q7P364      Protein translation elongation factor Tu (EF-TU)      394
   Q7P364_FUSNV [FNV2036]      AA
               [Fusobacterium nucleatum subsp. vincentii ATCC 49256] align

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Score = 567 bits (1462), Expect = e-160  
 Identities = 279/399 (69%), Positives = 326/399 (80%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRNTNPVHNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDIDNIDNAPQEKERG 60
      MAKEK+ R+ PNVNIGTIGHV HOKTT +AAIS VLS KGLA D+D ID AP+EKERG
Sbjct: 1  MAKEKYERSKPHVHNIGTIGHVDHGKTTTAAISKVLSKGLASKVDQIDAAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120
      ITI T+HIEYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI
Sbjct: 61  ITINTAHIEYETANRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120

Query: 121 LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+I+V+LNK + Y FPGD+ P++ GS+L AL
Sbjct: 121 LLSRQVGVPYIIIVYLNKADMVDDEELLELVEMEVRELLTEYGFPGDEIPVIRGSSLGALN 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
      + +W EK+++LM VDSYIPTPER ++ FLMP+ELVE+I GRGTVVTGR+ERG
Sbjct: 181 GEE-----KWIEKIMELMDAVDSYIPTPERAIDQFLMPIEDVFTITGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTGKKEEVERGMVLCK 300
      V+KVG+E+ELVGI+ T KTF TGVEMFRK L++G+AGDN+GVLLRGTGKKEEVERG VL K
Sbjct: 236 VIKVGEEIEIVGIKPTTKTTCTGVEMFRKLLDQGGAGDNIGVLLRGTGKKEEVERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
      PGSI PH F+ E+YVL+K+EGGRHTPFET YRPQFY RTTD+TG++TLP+GVEMVMPGD
Sbjct: 296 PGSIHPHTNFKGEVYVLTKEGGRHTPFFTGYRPOFYFRTTDTITGAVTLPDGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      N+ +TVELI P+A+E G +FAIREGGRTV +GVVS II+
Sbjct: 356 NITMTVELIHPIAMEQGLRFAIREGGRTVASGVVSEIIK 394

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tr Q7TTF9      Elongation factor tu, EF-Tu [tufA] [Haemophilus ducreyi] 394 AA
   Q7TTF9_HAEDU
                                           align

```

Score = 567 bits (1461), Expect = e-160  
 Identities = 279/399 (69%), Positives = 323/399 (80%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
        M+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG
Sbjct: 1  MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKHFGGAARAFDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI TSH+EY+TETRHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61  ITINTSHVEYDTETRHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LL RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+AL
Sbjct: 121  LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRSALQALN 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFIMPVEDVFSIAGRGT VVTGRIERG 240
        V EW EK+++L +DSYIP PER +K FL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 181  -----GVPEWEEKIIE LAQHLD SYIPEPERAIDKPFLLPIEDVFSISGRGT VVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        ++K G+EVEIVGI+ T KTTVTGVEMFRK L++G AG+NVG LLRGTK+EE+ERG VL K
Sbjct: 236  IIKSGEEVEIVGIKETT KTTVTGVEMFRKLLDEGRAGENVGALLRGTKREEIERGQVLAK 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360
        PG+ITPH FE E+YVLSKEEGGRHTPEF YRPQFY RTT DVTG+I LPEGVEMVMPGD
Sbjct: 296  PGTITPHTDFESEVYVLSKEEGGRHTPFFKGYRPQFYRTT DVTGTIELPEGVEMVMPGD 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
        N+K+TV LI P+A++ G +FAIREGGRTVGAGVV+ LI+
Sbjct: 356  NIKMTVSLIHPAMDEGLRFAIREGGRTVGAGVWAKIIE 394

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sp Q99QMO Elongation factor Tu (EF-Tu) [tufA] [Caulobacter 396
EFTU_CAUCR crescentus] AA
align

```

Score = 566 bits (1460), Expect = e-160  
Identities = 285/399 (71%), Positives = 323/399 (80%), Gaps = 3/399 (0%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
        MAKEKF RT PH NIGTIGHV HGKTTL+AAI+ L+ G A K YD ID AP+EK RG
Sbjct: 1  MAKEKFERTKPHCNIGTIGHVDHGKTTLTAAITMTLAKSGGATAKKYDEIDAAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI
Sbjct: 61  ITINTAHVEYETANRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LL+RQVGVP +VVF+NK S+Y+FPGDD PI GSAL A+E
Sbjct: 121  LLARQVGVPALVVF MNKVDMDDEELLELVEMEVRELLSSYQFPGDDIPITKGSALAAVE 180

Query: 181  EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFIMPVEDVFSIAGRGT VVTGRIERG 240
        + +GE EK+L+LMA VD+YIP PER + FIMPVEDVFSI+GRGT VVTGR+ERG
Sbjct: 181  -GRDPQIGE--EKILELMASVDAYIPQPERPVDMPFIMPVEDVFSISGRGT VVTGRVERG 237

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        +VVG+EVEIVGIR QKTT TGEMFRK L++G+AGDNVGVLLRGTK+E+VERG VLCK
Sbjct: 238  IVKVGEEVEIVGIRPVQKTTCTGVEMFRKLLDQGGAGDNVGVLLRGTKREDVERGQVLCK 297

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Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPPQFYVRTTDDVTGSITLPEGVEMVMPGD 360  
 PGSIPTPH KF E Y+L+KEEGGRHTPFFTNYRPPQFY RTTDDVTG I L EGVEN+MPGD  
 Sbjct: 298 PGSITPHTKFVAEAYILTKEEGGRHTPFFTNYRPPQFYRTTDDVTGIIKLREGVEMIMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 N ++ VELI+P+A+E +FAIREGGRTVGAGVV+ I+E  
 Sbjct: 358 NAELDVELITPIAMEEKLRFIREGGRTVGAGVVAKIVE 396

sp Q8Y422 Elongation factor Tu (EF-Tu) [tuf] [Listeria 395  
 EFTU\_LISMO monocytogenes] AA  
align

Score = 566 bits (1459), Expect = e-160  
 Identities = 277/398 (69%), Positives = 325/398 (81%), Gaps = 6/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKF+R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ KG A+ + YD ID AP+E+ERG  
 Sbjct: 1 MAKEKFDRSKPHVNIGTIGHVDHGKTTLTAAITTVLAKKGYADAQAYDQIDGAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI+T+H+EY+T++RHVAVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 61 ITISTAHVEYQTDNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP+IVVP+NK + YEFPGDD P++ GSAL+AL+  
 Sbjct: 121 LLSRQVGVPYIVVFMNKCMDVDEELLELVEMEIRDLLTEYEFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVTGRIERG 240  
 +W K+ +LM VDSYIPTPERDT+K F+MFVEDVEST GRGTV TGR+ERG  
 Sbjct: 181 -----GEADWEAKIDELMEAVDSYIPTPERDTEKTFMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 VVKVGDEVE++GI ++K VTGVEMFRK L+ EAGDN+G LLRG +E+++RG VL  
 Sbjct: 236 QVKVGDEVEVIGIEEESKKVVVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGVIA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPPQFYVRTTDDVTGSITLPEGVEMVMPG 359  
 KPGSITPH F+ E YVL+KEEGGRHTPF FTNYRPPQFY RTTDDVTG +TLPEG EMVMPG  
 Sbjct: 296 KPGSITPHTNFKAETYVLTKEEGGRHTPFFTNYRPPQFYRTTDDVTGIVTLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397  
 DN+++ VELI+P+A+E GTEK+IREGGRTVGAGVVSNI  
 Sbjct: 356 DNIELAVELIPIAIEDGTFKSIREGGRTVGAGVVSNI 393

sp Q71WB9 Elongation factor Tu (EF-Tu) [tuf] [Listeria monocytogenes 395 AA  
 EFTU\_LISMF (serotype 4b / strain F2365)]  
align

Score = 566 bits (1459), Expect = e-160  
 Identities = 277/398 (69%), Positives = 325/398 (81%), Gaps = 6/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKF+R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ KG A+ + YD ID AP+E+ERG  
 Sbjct: 1 MAKEKFDRSKPHVNIGTIGHVDHGKTTLTAAITTVLAKKGYADAQAYDQIDGAPEERERG 60

```

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120
           ITI+T+H+EY+T++RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI
Sbjct: 61  ITISTAHVEYQTDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
           LLSRQVGVP+IVVF+NK                      + YEFPGDD P++ GSAL+AL+
Sbjct: 121  LLSRQVGVPYIVVFMNKCMDVDEELLELVEMEIRDLLTEYEFPGDDIPVIKGSALKALQ 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
           +W K+ +LM VDSYIPTPERDT+K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  -----GEADWEAKIDELMEAVDSYIPTPERDTPKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
           VVKVGDEVE++GI ++K VTGVEMFRK L+ EAGDN+G LRG +E+++RG VL
Sbjct: 236  QVKVGDEVEVIGIEEESKVVVVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300  KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
           KPGSITPH F+ E YVL+KEEGGRHTFFF NYRPQFY RTTDTVG +TLPEG EMVMPG
Sbjct: 296  KPGSITPHTNFKAETYVLTKEEGGRHTPFFNNYRPQFYFRTTDTGIVTLPEGTEMVMPG 355

Query: 360  DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
           DN+++ VELL+P+A+E GTFK+IREGGRTVGAGVVSNI
Sbjct: 356  DNIELAVELIPIAIEDGTFKSIREGGRTVGAGVVSNI 393

```

sp. Q927I6      **Elongation factor Tu (EF-Tu) [tuf] [Listeria innocua]** 395 AA  
 EFTU\_LISIN

align

Score = 566 bits (1459), Expect = e-160

Identities = 277/398 (69%), Positives = 324/398 (80%), Gaps = 6/398 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
           MAKEKF+R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ KG A+ + YD ID AP+E+ERG
Sbjct: 1  MAKEKFDRSKPHVNIGTIGHVDHGKTTLTAAITTVLAKKGFADAQAYDQIDGAPEERERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120
           ITI+T+H+EY+T+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI
Sbjct: 61  ITISTAHVEYQTDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
           LLSRQVGVP+IVVF+NK                      + YEFPGDD P++ GSAL+AL+
Sbjct: 121  LLSRQVGVPYIVVFMNKCMDVDEELLELVEMEIRDLLTEYEFPGDDIPVIKGSALKALQ 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
           +W K+ +LM VDSYIPTPERDT+K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  -----GEADWEAKIDELMEAVDSYIPTPERDTPKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
           VVKVGDEVE++GI ++K VTGVEMFRK L+ EAGDN+G LRG +E+++RG VL
Sbjct: 236  QVKVGDEVEVIGIEEESKVVVVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300  KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
           KPGSITPH F+ E YVL+KEEGGRHTFFF NYRPQFY RTTDTVG +TLPEG EMVMPG
Sbjct: 296  KPGSITPHTNFKAETYVLTKEEGGRHTPFFNNYRPQFYFRTTDTGIVTLPEGTEMVMPG 355

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Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397  
 DN+++ VELL+P+A+E GTKF+IREGGRTVGAGVVSNI  
 Sbjct: 356 DNIELAVELIPIAIEDGTKFSIREGGRTVGAGVVSNI 393

tr Q81ZS3 GTPases-translation elongation factors and sulfate 396  
 Q81ZS3\_NITEU adenylate AA  
 transferase subunit 1 (EC 3.6.1.48) [tuf2] [Nitrosomonas align  
 europaea]

Score = 565 bits (1457), Expect = e-160  
 Identities = 280/399 (70%), Positives = 324/399 (81%), Gaps = 3/399 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAK KF R PHVN+GTIGHV HGKTTL+AAI+ +L+ K E K YD ID+AP+E+ RG  
 Sbjct: 1 MAKSKFERVVKPHVNVGTIGHVDHGKTTLTAAITTLTKKFGGEAKSYDQIDSAPEERARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI TSH+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI  
 Sbjct: 61 ITINTSHVEYETDKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVE+I+VF+NK S Y+FPGDDTPI+ GSAL+ALE  
 Sbjct: 121 LLARQVGVPYIIVFMNKADMVDDAELELVEMEIRELLSNYDFPGDDTPIIIGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVTGRIERG 240  
 K+ ++GE +LKL +DSYIP PER + F+MPVEDVFSI+GRGTVVTGR+ERG  
 Sbjct: 181 GDKS-DIGE--AAILKLAEALDSYIPEPERAIDGAFIMPVEDVFSISGRGTVVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 +VKGDE+ELVG++ T RT TGVEMFRK L++G+AGDNVG+LLRGTK+EEVERG VL K  
 Sbjct: 238 IVKVGDEIEIVGLKPTIKTVCTGVEMFRKLLDQGQAGDNVGIILLRGTKREEVERGQVLAK 297

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTVTSITLPEGVEMVMPGD 360  
 PGSI PH KF ELYVLSKEEGGRHTPFF YRPQFY RTTDTVTSI LP GVEMVMPGD  
 Sbjct: 298 PGSILPHTKFTAIEIYVLSKEEGGRHTPFFAGYRPQFYFRTTDTVTSIELPAGVEMVMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 N+ +TV LI+P+A++ G +FAIREGGRTVGAGVV+ +IE  
 Sbjct: 358 NISVTVNLIPIAMDEGLRFAIREGGRTVGAGVVAKVIE 396

sp P57939 Elongation factor Tu-A (EF-Tu-A) [tufA] [Pasteurella 394  
 EFTU1\_PASMU multocida] AA  
align

Score = 565 bits (1456), Expect = e-160  
 Identities = 277/399 (69%), Positives = 323/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 M+KEKE RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG  
 Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKHYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120



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      ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL RQVGVP+I+VFLNK                      S Y+FPGDDTPIV GSAL+AL
Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALQALN 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      V EW EK+L+L +D+YIP P+R ++ EL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 181 -----GVAEWEKILELANHLDTYIPEPQRAIDQPFLPIEDVFSISGRGT VVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +++ G+VEVEIVGI+AT KTTVTGVEMERK L++G AG+NVG LLRGTK+EE+ERG VL K
Sbjct: 236 IIRTGEEVEIVGIKATTKTTVTGVEMFRKLLDEGRAGENVGALLRGTKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYPQFYVRTTDTG SITLPEGVEMVMPGD 360
      PGSITPH FE E+YVLSKEEGGRHTPFF YRPQFY RTTDTG+I LPEGVEMVMPGD
Sbjct: 296 PGSITPHTDFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTTDTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      N+K+TV LI P+A++ G +FAIREGGRTVGAGVV+ II+
Sbjct: 356 NIKMTVSLIHPAMDQGLRFAIREGGRTVGAGVVAKIIE 394

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tr Q65QG6      TufB protein [tufB] [Mannheimia succiniciproducens] 394
Q65QG6_MANSM (strain AA
MBEL55E) ] align

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Score = 565 bits (1455), Expect = e-160  
Identities = 276/399 (69%), Positives = 322/399 (80%), Gaps = 5/399 (1%)

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Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      M+KEKE RT PHVN+GTIGHV HGKTTLSAAI+ VLS + +D IDNAP+EK RG
Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLSKHYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL RQVGVP+I+VFLNK                      S Y+FPGDDTPIV GSAL+ALE
Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      +W EK+L+L +D+YIP PER ++ EL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 181 -----GEAQWEEKILELANALDXYIPEPERAIDQPFLPIEDVFSISGRGT VVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +++ GDEVEIVGI+ T KTTVTGVEMERK L++G AG+N+G LLRGTK+EE+ERG VL K
Sbjct: 236 IIRTGDEVEIVGIKETAKTTVTGVEMFRKLLDEGRAGENIGALLRGTKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYPQFYVRTTDTG SITLPEGVEMVMPGD 360
      PGSITPH FE E+YVLSKEEGGRHTPFF YRPQFY RTTDTG+I LPEGVEMVMPGD
Sbjct: 296 PGSITPHTDFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTTDTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399

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N+K+TV LI P+A++ G +FAIREGGRTVGAGVV+ II+  
 Sbjct: 356 NIKMTVSLIHPIAMDQGLRFAIREGGRTVGAGVVAKIHK 394

tr Q8L160 **Elongation factor Tu [tufA] [Myxococcus** 396 AA  
Q8L160\_MYXA **xanthus]** align

Score = 565 bits (1455), Expect = e-160  
 Identities = 283/400 (70%), Positives = 324/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKF R PHVNIGTIGHV HGKT+L+AAI+ VL+ G A YD ID AP+E+ERG  
 Sbjct: 1 MAKEKFNRTNPHVNIGTIGHVDHGKTSITAAITKVLAKTGGATFLAYDLIDKAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI+TSH+EY+T RHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI  
 Sbjct: 61 ITISTSHVEYQTSNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP+IVVFLNK YEFPDGD PI+ GSAL+ALE  
 Sbjct: 121 LLARQVGVPPIVFLNKVDMLDDPELRELVEMEVRDLLKKYEFPGDDIPIPGSALKALE 180

Query: 181 EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIER 239  
 G+ + GE +LKLM VDSYIPTP+R T+K FLMPVEEDVFSI+GRGTV TGR+ER  
 Sbjct: 181 ----GDTSDIGEPAILKLMEAVDSYIPTPQRATDKPFLMPVEDVFSISGRGTVATGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 G++KVG+EVE+VG+R TQKT VTGVEMFRK L++G AGDN+G L+RG K+E++ERG VL  
 Sbjct: 237 GIIKVGEEVEVGLRPTQKTTVTGVEMFRKLLDQGMAGDNIGALVRGLKREDMERGQVLA 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDVTGSITLPEGVEMVMPG 359  
 KPGSITPH KF+ +IYVLSKEEGGRHTPFF YRPQFY RTTDVTGS+ LPE VEMVMPG  
 Sbjct: 297 KPGSITPHTKFKAQIYVLSKEEGGRHTPFFKGYRPFYFRTTDVTGSVKLPENVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DN+ I VELT+PVA+E +PA+REGGRTVGAGVV+ IIE  
 Sbjct: 357 DNIAIEVELITPVAMEKELRFAVREGGRTVGAGVVAEIIIE 396

tr Q5FTY1 **Protein Translation Elongation Factor Tu (EF-TU)** 396  
Q5FTY1\_GLUOX **[GOX0382]** AA  
**[Gluconobacter oxydans (Gluconobacter suboxydans)]** align

Score = 564 bits (1454), Expect = e-159  
 Identities = 281/397 (70%), Positives = 326/397 (81%), Gaps = 3/397 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF RT PH NIGTIGHV HGKT+L+AAI+ VL+ G A YD ID AP+E+ RG  
 Sbjct: 1 MAKAKFERTKPHCNIGTIGHVDHGKTSITAAITKVLAKTGGATYSAYDQIDKAPEERARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI+T+R+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI  
 Sbjct: 61 ITISTAHVEYETADRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180

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      LL+RQVGVP +VVFLNK                      S+Y+FPGDD PIV GSAL LE
Sbjct: 121 LLARQVGVPALVVFLNKVDQVDDPELLELVEMEVRRELLSSYQFPGDDIPIVKGSALVTLE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      +   ++GE ++VL+LM +VD+YIP PER ++ FIMP+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181 DGDP-SIGE--DRVLELMTQVDAYIPQPERPVDRPFLMPIEDVFSISGRGTVVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      VV VGDEVEIVG++ T KTTVTGVEMFRK L++GEAGDN+G L+PGTK+E+VERG VL K
Sbjct: 238 VVNVGDEVEIVGLKDTVKTVTGVEMFRKLLDRGEAGDNIGALVRGTRKREDVERGQVLAK 297

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPGD 360
      PGSITPHKKF+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTDTG +TLPEG EMVMPGD
Sbjct: 298 PGSITPHKKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTTDTGVVTLPEGTEMVMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
      NV + VELI+P+A++ G +FAIREGGRTVGAGVVS+I
Sbjct: 358 NVAMDVELIAPIAMDEGLRFAIREGGRTVGAGVVSSI 394

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sp Q8ETY4      Elongation factor Tu (EF-Tu) [tuf] [Oceanobacillus      395
  EFTU_OCEIH iheyensis]      AA
                               align

```

Score = 564 bits (1453), Expect = e-159  
 Identities = 279/398 (70%), Positives = 322/398 (80%), Gaps = 6/398 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      MAKEK+K+ HVN+GT+GHV HGKTTL+AAI+ VL+ G E + YD ID AP+E+ERG
Sbjct: 1  MAKEKFRDSKSHVNVGTLGHVDHGKTTLTAAITTVIAKHGGGEARAYDQIDGAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LLSR VGVP VVFLNK                      + Y+FPGDD P++ GSAL+ALE
Sbjct: 121 LLSRNVGVPAPVVFLNKTDMDVDEELLELVEMEVRDLLTEYDFPGDDLPIVKGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      V E+ E++L+IMA VD YIPTPERD EK F+MPVEDVEST GRGTV TGR+ERG
Sbjct: 181 -----GVAEYEERILELMAAVDEYIPTPERDKEKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      VVKVGDEVET+G+ KTTVTGVEMFRK L+ EAGDN+G LLRG +E++ RG VL
Sbjct: 236 EVKVGDEVEIIGLAEDASKTTVTGVEMFRKLLDYAEAGDNIGALLRGVSREDINRGQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPG 359
      KPGSITFH F+ E+YVLSKEEGGRHTPFFT+NYRPQFY RTTDTG I LPFG EMVMPG
Sbjct: 296 KPGSITPHTNFKAENVVLSKEEGGRHTPFFSNYRPQFYFRTTDTGVIELPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397
      DN+++TVELISP+A+E GT+F+IREGGRTVG+GVVS+I
Sbjct: 356 DNIEMTVELISPIAIEDGTRFSIREGGRTVGSGVVSSI 393

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tr Q605B0 Translation elongation factor Tu [tuf-2] [Methylococcus 396  
 Q605B0\_METCA capsulatus] AA  
align

Score = 563 bits (1452), Expect = e-159  
 Identities = 279/400 (69%), Positives = 326/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIQTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 M+KEKE RT PHVN+GTIGHV HGKTTL+AA++ ++ K E K YD ID AP+E+ RG  
 Sbjct: 1 MSKEKFTRTKPHVNVGTIGHVDHGKTTTLTAALTKCMAAKFGGEFKAYDQIDAAPEERARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITIAT+H+EYE+ RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 61 ITIATAHVEYESAARHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP+IVVFLNK S Y+FPGDD PI+ GSAL+ALE  
 Sbjct: 121 LLARQVGVPPIVFLNKADMVDDPELLELVEMEVRELLSKYDFPGDDIPIIKGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AE-VDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIER 239  
 G+ E G ++ + + +D YIP PER ++ FLMP+EDVFSI+GRGTVVTGR+ER  
 Sbjct: 181 ----GDGSEIGVPAVEALVQALDDYIPEPERAIDRPFMLPIEDVFSISGRGTVVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 G++KVG+E+EIIVGIR T KTT TGVEMFRK L++G+AGDN+GVLLRGTK+E+VERG VL  
 Sbjct: 237 GIIKVGEEIEIVGIRPTAKTTCTGVEMFRKLLDQGGAGDNIGVLLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVTSITLPEGVEMVMPG 359  
 KPGSITPH FE EIVVLSKEEGGRHTPEE YRPQFY RTTDTVIG++TLPEGVEMVMPG  
 Sbjct: 297 KPGSITPHTHFEAEIYVLSKEEGGRHTPFFNGYRPQFYFRTTDTVTAATLPEGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNVKI V+LI+P+A++ G +PA+REGGRTVGAGVVS ILE  
 Sbjct: 357 DNVKIEVKLIAPIAMDEGLRFAVREGGRTVGAGVVSNIIE 396

tr Q8EK70 Translation elongation factor Tu [tufA] [Shewanella 394  
 Q8EK70\_SHEON oneidensis] AA  
align

Score = 563 bits (1450), Expect = e-159  
 Identities = 278/398 (69%), Positives = 320/398 (79%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIQTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAK KE R+ PHVN+GTIGHV HGKTTL+AAIS VL+ E KD+ IDNAP+E+ERG  
 Sbjct: 1 MAKAKFERSKPHVNVGTIGHVDHGKTTTLTAASHVLAKTYGGEAKDFSQIDNAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI TSHIEY+T +RHYAHVDCPGHADVKNMITGAAQMDGAILVV++ DGMPQTREHI  
 Sbjct: 61 ITINTSHIEYDTPSRHYAHVDCPGHADVKNMITGAAQMDGAILVVASTDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP I+VF+NK S Y+FPGDD P++ GSAL+ALE  
 Sbjct: 121 LLSRQVGVPFIIVFMNKCDDMVDDAELELVEMEVRELLSEYDFPGDDLPVIQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240  
 EW K+L+L A +DSYIP PERD +K FLMP+EDVFSI+GRGTVVTGR+ERG

Sbjct: 181 GEP-----EWEAKILELAAALDSYIPEPERDIDKPFLMPIEDVFSISGRGTVVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 +V+VGDEVEIVGIR T KTT TGVEMFRK L++G AG+N G+LLRGTK+++VERG VL K

Sbjct: 236 IVRVGDEVEIVGIRTTTCTCTGVEMFRKLLDEGRAGENC GILLRGTKRDDVERGQVLSK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPOFYVRTTDDVTGSITLPEGVEMVMPGD 360  
 PGSI PH FE E+YVLSKEEGGRHTPFF YRPOFY RTTDDVTG+I LPEGVEMVMPGD

Sbjct: 296 PGSINPHTTFESEVYVLSKEEGGRHTPFFKGYRPOFYFRTTDDVTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398  
 N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ II

Sbjct: 356 NIKMVTLICPIAMDEGLRFAIREGGRTVGAGVVAKII 393

tr Q7TT91 **Elongation factor Tu [tufA] [Bordetella** 396 AA  
Q7TT91\_BORPE **pertussis]** align

Score = 563 bits (1450), Expect = e-159  
 Identities = 285/400 (71%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K E + YD ID AP+EK RG

Sbjct: 1 MAKGKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLSNKFGEARGYDQIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI TSH+EXETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI

Sbjct: 61 ITINTSHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP+I+VELNK S Y+FPGDDTPIV GSA ALE

Sbjct: 121 LLSRQVGVPYIIIVFLNKADMVDDAELELVEMEVRELLSKYDFPGDDTPIVKS AKLALE 180

Query: 181 EAKAGNVGEWGEK-VLKILMAEVD SYIPTPERDTEKTF LMPVEDVFSIAGRGTVVTGRIER 239  
 G+ GE GE+ +L L +D+YIPTPER + FLMPEVDVFSI+GRGTVVVTGRIER

Sbjct: 181 ----GDKGELGEQAILS LAQALDYIPTPERAVDGAFLMPVEDVFSISGRGTVVVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 GVVKVG+E+IVGI+ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL

Sbjct: 237 GVVKVGEEIEIVGIKPTVKTCTCTGVEMFRKLLDQGGAGDNV GILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPOFYVRTTDDVTGSITLPEGVEMVMPG 359  
 KPGSI PH F E+Y+LSKEEGGRHTPFF YRPOFY RTTDDVTG+I LP EMV+PG

Sbjct: 297 KPGSINPHTDFTA EVYILSKEEGGRHTPFFNGYRPOFYFRTTDDVTGTIDL PADKEMVLPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV +TV+L++P+A+E G +FAIREGGRTVGAGVV+ II+

Sbjct: 357 DNVSM TVKLLAPIAMEEGLRFAIREGGRTVGAGVVAKIIK 396

tr Q79GC6 **Elongation factor Tu [tuf] [Bordetella parapertussis]** 396 AA  
Q79GC6\_BORPA align

Score = 563 bits (1450), Expect = e-159

Identities = 285/400 (71%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K   E + YD ID AP+EK RG
Sbjct: 1  MAKGKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLSNKFGEARGYDQIDAAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI TSH+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI
Sbjct: 61  ITINTSHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+I+VFLNK                               S Y+FPGDDTPIV GSA ALE
Sbjct: 121  LLSRQVGVPYIIIVFLNKADMVDDAELLELVEMEVRELLSKYDFPGDDTPIVKGSAKLAL 180

Query: 181  EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239
      G+ GE GE+ +L L   +D+YIPTPER +   FILMPVEDVFSI+GRGTVVTGRIER
Sbjct: 181  ----GDKGELGEQAILSQAQALDTYIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240  GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      GVVKVG+E+EI VGI+ T KTT TGVEMFRK L++G+AGENVG+LLRGTK+E+VERG VL
Sbjct: 237  GVVKVGEEIEIVGIKPTVKTCTGVEMFRKLLDQGGAGDNVGIILLRGTKREDVERGQVLA 296

Query: 300  KPGSITPHKKFEEIEIVLSKEEGGRHTPFFTNYRPQFYVRTTDTVTSITLPEGVEMVMPG 359
      KPGSI PH F   E+Y+LSKEEGGRHTFFF YRFQFY RTTDTG+I LF   EMV+FG
Sbjct: 297  KPGSINPHTDFTAENVYILSKEEGGRHTPFFNGYRPQFYFRTTDTGTIDLPAKEMVLP 356

Query: 360  DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNV +TV+L++P+A+E G +FAIREGGRTVGAGVV+ II+
Sbjct: 357  DNVSMTVKLLAPIAMEEGLRFAIREGGRTVGAGVVAKI 396

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tr Q79G84      Elongation factor Tu [tuf] [Bordetella bronchiseptica] 396
Q79G84_BORBR  (Alcaligenes bronchisepticus)] AA
align

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Score = 563 bits (1450), Expect = e-159

Identities = 285/400 (71%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VLS K   E + YD ID AP+EK RG
Sbjct: 1  MAKGKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLSNKFGEARGYDQIDAAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI TSH+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI
Sbjct: 61  ITINTSHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+I+VFLNK                               S Y+FPGDDTPIV GSA ALE
Sbjct: 121  LLSRQVGVPYIIIVFLNKADMVDDAELLELVEMEVRELLSKYDFPGDDTPIVKGSAKLAL 180

Query: 181  EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239
      G+ GE GE+ +L L   +D+YIPTPER +   FILMPVEDVFSI+GRGTVVTGRIER
Sbjct: 181  ----GDKGELGEQAILSQAQALDTYIPTPERAVDGAFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240  GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      GVVKVG+E+EI VGI+ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL

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Sbjct: 237 GVVKGVEEIEIVGIKPTVKTCTGVEMFRKLLDQGGAGDNVIGILLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFFTNYRPPQFYVRTTDVTGSITLPEGVEMVMPG 359  
 KPGSI PH F E+Y+LSKEEGGRHTFFF YRPQFY RTTDTG+I LF EMV+PG

Sbjct: 297 KPGSINPHTDFTAENVYILSKEEGGRHTPFFNGYRPPQFYRTTDTGTIDLPADKEMVLPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV +TV+L++P+A+E G +FAIREGGRTVGAGVV+ II+

Sbjct: 357 DNVSMTVKLLAPIAMEEGLRFAIREGGRTVGAGVVAKIIE 396

tr Q5GWR8 Elongation factor Tu [tufB] [*Xanthomonas oryzae* (pv. 396  
 Q5GWR8\_XANOR *oryzae*)] AA  
align

Score = 563 bits (1450), Expect = e-159  
 Identities = 281/400 (70%), Positives = 327/400 (81%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF RT PHVN+GTIGHV HGKTTL+AA++ + + + E K YD ID AP+EK RG

Sbjct: 1 MAKAKFERTKPHVNVGTIGHVDHGKTTLTAAITKIGAERFGGEFKAYDAIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVSAADGMPQTREHI 120  
 ITI+T+H+EYE+ +HYAHVDCPGHADVKNMITGAAQMDGAILV SAADGMPQTREHI

Sbjct: 61 ITISTAHVEYESPSRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVPPIVFLNK S Y+EPGDDTPI+ GSA AL+

Sbjct: 121 LLSRQVGVPPIVFLNKADMVDDAELELVEMEVRRELLSKYDFPGDDTPIIHGSARLALD 180

Query: 181 EAKAGNVGEWG-EKVLKLMAEVD SYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIER 239  
 G+ E G +LKL+ +D++IP P RD ++ FLMPVEDVFSI+GRGTVVTGRIER

Sbjct: 181 ----GDQSEIGVPAILKLVDALDTFIPEPTRDVRPFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240 GVVKGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 G++KVGDE+EIVGIRATQKTTVTGVEMFR L++G+AGDN G+LLRGTK+++VERG VLC

Sbjct: 237 GIIKVGDEIEIVGIRATQKTTVTGVEMFRKLLDQGGAGDNAGLLLRGTRDDVERGQVLC 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFFTNYRPPQFYVRTTDVTGSITLPEGVEMVMPG 359  
 KPGSI PH +FE E+YVLSK+EGGRHTFFF YRPQ Y RTTDTG+I LPEGVEMVMPG

Sbjct: 297 KPGSIKPHTFEAEVYVLSKDEGGGRHTPFFKGYRPPQLYFRTTDTITGAIDLPEGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNVK+TV LI+EVA++ G +FAIREGGRTVGAGVVS II+

Sbjct: 357 DNVKMTVTLINPVAMDEGLRFAIREGGRTVGAGVVSIIIE 396

sp P43926 Elongation factor Tu (EF-Tu) [tufA] [*Haemophilus* 393  
 EFTU\_HAEIN *influenzae*] AA  
align

Score = 562 bits (1448), Expect = e-159  
 Identities = 275/398 (69%), Positives = 321/398 (80%), Gaps = 5/398 (1%)

Query: 2 AKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERGI 61

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+KEKEF RT PHVN+GTIGHV HGKTTT+AAI+ VL+      + +D IDNAP+EK RGT
Sbjct: 1  SKEKFERTKPHVNVGTIGHVDHGKTTTAAITTVLAKHYGGAARAFDQIDNAPEEKARGI 60

Query: 62  TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHIL 121
          TT TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQTREHIL
Sbjct: 61  TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPQTREHIL 120

Query: 122  LSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 181
          L RQVGVP+I+VFLNK                      S Y+FPGDDTPIV GSAL+AL
Sbjct: 121  LGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRLLSQYDFPGDDTPIVRGSALQALN- 179

Query: 182  AKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 241
          V EW EK+L+L +D+YIF PER ++ FL+P+EDVFSI+GRGTVVTGR+ERG+
Sbjct: 180  ----GVAEWEKILELANHLDTYIPEPERAIDQPFLLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242  VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301
          ++ GDEVEIVGI+ T KTTVTGVEMFRK L++G AG+N+G LLRGT+EE+ERG VL KP
Sbjct: 236  IRTGDEVEIVGIKDTAKTTVTGVEMFRKLLDEGRAGENIGALLRGTKREEIERGQVLAKP 295

Query: 302  GSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGTSITLPEGVEMVMPGDN 361
          GSITPH FE E+YVLSK+EGGRHTPFF YRPQFY RTTDTGT+I LPEGVEMVMPGDN
Sbjct: 296  GSITPHTDFESEVYVLSKDEGGRHTPFFKGYRPQFYFRTTDTGTIELPEGVEMVMPGDN 355

Query: 362  VKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
          +K+TV LI P+A++ G +FAIREGGRTVGAGV+ II+
Sbjct: 356  IKMTVSLIHPAMDQGLRFAIREGGRTVGAGVVAKIIE 393

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sp P57966      Elongation factor Tu-B (EF-Tu-B) [tufB] [Pasteurella] 394
EFTU2_PASMU multocida] AA
align

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Score = 561 bits (1447), Expect = e-159  
Identities = 275/399 (68%), Positives = 322/399 (79%), Gaps = 5/399 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
          M+KEKEF RT PHVN+GTIGHV HGKTTT+AAI+ VL+      + +D IDNAP+EK RG
Sbjct: 1  MSKEKFERTKPHVNVGTIGHVDHGKTTTAAITTVLAKHYGGAARAFDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
          ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61  ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
          LL RQ+GV +I+VFLNK                      S Y+FPGDDTPIV GSAL+AL
Sbjct: 121  LLGRQIGVAYIIVFLNKCDMVDDEELLELVEMEVRLLFSQYDFPGDDTPIVRGSALQALN 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFLMPVEDVFSIAGRGTVVTGRIERG 240
          V EW EK+L+L +D+YIF P+R ++ FL+P+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181  -----GVAEWEKILELANHLDTYIPEPQRAIDQPFLLPIEDVFSISGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
          +++ G+VEVEIVGI+AT KTTVTGVEMFRK L++G AG+N+G LLRGT+EE+ERG VL K
Sbjct: 236  IIRTGEEVEIVGIKATKTTVTGVEMFRKLLDEGRAGENVGALLRGTKREEIERGQVLAK 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGTSITLPEGVEMVMPGD 360

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POSITPR FE E+YVLSKEEGGRATPEE YRPQFY RTTDVTG+I LPEGVEMVMPGD  
 Sbjct: 296 PGSITPHTDFESEVYVLSKEEGGRHTPFFKGYRPFYFRTTDDVTGTIELPEGVEMVMPGD 355  
 Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 N+K+TV LI P+A++ G +FAIREGGRTVGAGVV+ LI+  
 Sbjct: 356 NIKMTVSLIHPIAMDQGLRFAIREGGRTVGAGVVAKIIE 394

tr Q65PA9 TufA (Elongation factor Tu) [tufA] [Bacillus 396  
 Q65PA9\_BACLD licheniformis (strain AA  
 DSM 13 / ATCC 14580)] align

Score = 561 bits (1447), Expect = e-159  
 Identities = 281/401 (70%), Positives = 326/401 (81%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLK-GLAEMKDYDNIDNAPQEKER 59  
 MAKEKFF+R+ R NIGTIGHV HGKTTL+AAI+ VL K G YD ID AP+E+ER  
 Sbjct: 1 MAKEKFDRSKSHANIGTIGHVDHGKTTLTAAITTVLHKKSGKGTAMAYDQIDGAPEERER 60

Query: 60 GITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREH 119  
 GITI+P+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREH  
 Sbjct: 61 GITISTAHVEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREH 120

Query: 120 ILLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRAL 179  
 ILLSR VGVP+IVVFLNK S YEFPGDD P++ GSAL+AL  
 Sbjct: 121 ILLSRNVGVPPIVFLNKCDMVDDEELLELVEMEVRDLLSEYEFPGDDVPVIKGSALKAL 180

Query: 180 EEAKAGNVGEWGEKVLKMAEVD SYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239  
 E ++ EK+ +LMA VD YIPPER+T+K F+MPVEDVFSI GRGTV TGR+ER  
 Sbjct: 181 E-----GDAQYEEKIFELMAAVDEYIPTPERETDKPFMPVEDVFSITGRGTVATGRVER 235

Query: 240 GVVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298  
 G VKVGDEVEI+G++ +KTTVTGVEMFRK L+ EAGDN+G LLRG +EE++RG VL  
 Sbjct: 236 GQVKVGDEVEIIGLQENKKTTVTGVMFRKLLDYAEAGDNIGALLRGVSREEIQRGQVL 295

Query: 299 CKPGSITPHKKFEEEEIYVLSKEEGGRHTPFFFTNYRPFYFRTTDDVTGSITLPEGVEMVMP 358  
 +PG+ITPHKKF+ E+YVLSKEEGGRHTPFF+NYRPFY RTTDVTG I LPEGVEMVMP  
 Sbjct: 296 AQPGTITPHKKFKAENVYVLSKEEGGRHTPFFSNYRPFYFRTTDDVTGIIQLPEGVEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 GDN+++TVELIS +A+E GT+F+IREGGRTVG+GVVS+IIE  
 Sbjct: 356 GDNIMTVELISTIAIEDGTRFSIREGGRTVGSGVVSIIIE 396

sp P33169 Elongation factor Tu (EF-Tu) [tuf] [Shewanella 394  
 EFTU\_SHEPU putrefaciens AA  
 (Pseudomonas putrefaciens)] align

Score = 561 bits (1445), Expect = e-158  
 Identities = 276/398 (69%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAK KF R PHVN+GTIGHV HGKTTL+AAIS VL+ E KD+ IDNAP+E+ERG  
 Sbjct: 1 MAKAKFERIKPHVNVGTIGHVDHGKTTLTAAISHVLAKTYGGEAKDFSQIDNAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI TSHIEY+T +RHYAHVDCPGHADYVKNMITGAAQMDGAILVV++ DGMPQTREHI  
 Sbjct: 61 ITINTSHIEYDTPSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVASTDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP I+VF+NK S Y+FPGDD P++ GSAL+ALE  
 Sbjct: 121 LLSRQVGVPFIIVFMNKCDDVDEELLELVEMEVRELLSEYDFPGDDLPIVQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240  
 EW K+L+L A +DSYIP P+RD +K FL+P+EDVESI+GRGTVVTGR+ERG  
 Sbjct: 181 GEP-----EWEAKILELAAALDSYIPEPQRDIDKPFLLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 +V+VGDEVEIVG+RAT KTT TGVEMFRK L++G AG+N G+LLRGTK+++VERG VL K  
 Sbjct: 236 IVRVGDEVEIVGVRATTKTTCTGVEMFRKLLDEGRAGENC GILLRGTKRDDVERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTG SITLPEGVEMVMPGD 360  
 PGSI PH FE E+YVLSKEEGGRHTPFF YRPQFY RTTDTGT+I LPEGVEMVMPGD  
 Sbjct: 296 PGSINPHTTFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTTDTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398  
 N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ II  
 Sbjct: 356 NIKMVVTLICPIAMDEGLRFAIREGGRTVGAGVAKII 393

tr Q8EK81 Translation elongation factor Tu [tufB] [Shewanella] 394  
Q8EK81\_SHEON oneidensis AA  
align

Score = 561 bits (1445), Expect = e-158

Identities = 277/397 (69%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAK KE R+ PHVN+GTIGHV HGKTTLSAAIS VL+ E KD+ IDNAP+E+ERG  
 Sbjct: 1 MAKAKFERSKPHVNVGTIGHVDHGKTTLTAAISHVLAKTYGGEAKDFSQIDNAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI TSHIEY+T +RHYAHVDCPGHADYVKNMITGAAQMDGAILVV++ DGMPQTREHI  
 Sbjct: 61 ITINTSHIEYDTPSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVASTDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP I+VF+NK S Y+FPGDD P++ GSAL+ALE  
 Sbjct: 121 LLSRQVGVPFIIVFMNKCDDVDAELLELVEMEVRELLSEYDFPGDDLPIVQGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240  
 EW K+L+L A +DSYIP PERD +K FLMP+EDVESI+GRGTVVTGR+ERG  
 Sbjct: 181 GEP-----EWEAKILELAAALDSYIPEPERDIDKPFLLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 +V+VGDEVEIVGIR T KTT TGVEMFRK L++G AG+N G+LLRGTK+++VERG VL K  
 Sbjct: 236 IVRVGDEVEIVGIRTTTCTGVEMFRKLLDEGRAGENC GILLRGTKRDDVERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTG SITLPEGVEMVMPGD 360  
 PGSI PH FE E+YVLSKEEGGRHTPFF YRPQFY RTTDTGT+I LPEGVEMVMPGD  
 Sbjct: 296 PGSINPHTTFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTTDTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397  
 N+K+ V LL P+A++ G +FAIREGGRTVGAGVV+ I  
 Sbjct: 356 NIKMKVTLICPIAMDEGLRFAIREGGRTVGAGVVAKI 392

tr Q5NQ65 Translation elongation factor [ZM00516] [Zymomonas 397  
 Q5NQ65\_ZYMMO mobilis] AA  
align

Score = 561 bits (1445), Expect = e-158  
 Identities = 283/400 (70%), Positives = 326/400 (80%), Gaps = 4/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAE-MKDYNIDNAPQEKER 59  
 MAK KF R PH NIGTIGHV HGKTTL+AAI+ VL+ G DY NID AP+E+ER  
 Sbjct: 1 MAKAKFERNKPHCNIGTIGHVDHGKTTLTAAITKVLAEEAGGGNTFVDYANIDKAPEERER 60

Query: 60 GITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREH 119  
 GITI+TSH+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREH  
 Sbjct: 61 GITISTSHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREH 120

Query: 120 ILLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRAL 179  
 ILL+RQVGVP +VVF+NK S+Y+FPGDD PIV GSAL AL  
 Sbjct: 121 ILLARQVGVPALVVFMMNKVDQVDDPELLELVEMEIRELLSSYDFPGDDIPIVKGSALAAL 180

Query: 180 EEAKAGNVGEWGEKVLKILMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239  
 E+ K +G+ E +L LMA VD YIP PER +K+FLMP+EDVFSI+GRGTVVTGR+E  
 Sbjct: 181 ED-KNPEIGK--EAILSLMAAVDEYIPQPERPLDKSFLMPIEDVFSISGRGTVVTGRVET 237

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 G+VKVG+EVEIVG+R T+KTTVTGVEMFRK L++G+AGDN+G LLRGT + EVERG VL  
 Sbjct: 238 GIVKVGEEVEIVGLRDTKKTVTGVEMFRKLLDQGGAGDNIGALLRGARTEVERGQVLA 297

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPOFYVRTTDTVGSITLPEGVEMVMPG 359  
 KPGSITPH +F+ E+YVLSK+EGGRHTPFF NYRFQFY RTTDTVG ITLFE VEMVMPG  
 Sbjct: 298 KPGSITPHTEFKAEVYVLSKDEGGRHTPFFANYRPOFYFRTTDTVGEITLPEDVEMVMPG 357

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DN+ V+LI+P+A++ G +FAIREGGRTVGAGVVS+II+  
 Sbjct: 358 DNIAFGVKLIAPIAMDPGLRFAIREGGRTVGAGVVSIIK 397

sp Q8CQ81 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus 394  
 EFTU\_STAEP epidermidis] AA  
align

Score = 560 bits (1444), Expect = e-158  
 Identities = 276/399 (69%), Positives = 320/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKF+R+ H NIGTIGHV HGKTTL+AAI+ VL+ G + YD IDNAP+EKERG  
 Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDTVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120  
 ITI T+HIEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG ILVVSADGMPMPQTREHI  
 Sbjct: 61 ITINTAHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSADGMPMPQTREHI 120

Query: 121 LLSRQVGVP HIVVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSR VGVP +VVELNK S Y+FPGDD P++AGSAL+ALE  
 Sbjct: 121 LLSRNVGPALVVFLNKVDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240  
 E+ +K+L IM VD YITPERD++K F+MPVEDVFSI GRGTV TGR+ERG  
 Sbjct: 181 -----GDAEYEQKILDLMQAVDDYIPTPERDS DKPFMPVEDVFSITGRGT VATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 +KVG+EVEL+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL  
 Sbjct: 236 QIKVGEEVEIIGMHETS KTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLA 295

Query: 301 PGSITPHKKFEEIYVLSKEEGRHTPFFTNYR PQFYVRTT DVTGSITLPEGVEMVMPGD 360  
 PGSITPH KF+ E+YVLSK+EGGRHTPFFTNYR PQFY RTTDTG + LPEG EMVMPGD  
 Sbjct: 296 PGSITPHTKFKA EYVLSKDEGGRHTPFFTNYR PQFYFR TTDVTGVVNLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ I E  
 Sbjct: 356 NVENTVELI APIAIEDGTRFSIREGGRTVGSGVVTEIFE 394

sp P33167 Elongation factor Tu (EF-Tu) [tuf] [Burkholderia cepacia] 396 AA  
 EFTU\_BURCE (Pseudomonas cepacia)]

align

Score = 560 bits (1444), Expect = e-158  
 Identities = 282/400 (70%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAK KF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ K E K YD ID AP+EK RG  
 Sbjct: 1 MAKGKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLTKKFGGEAKAYDQIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120  
 ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILV SAADGMPMPQTREHI  
 Sbjct: 61 ITINTAHVEYETANRHYAHVDCPGHADVKNMITGAAQMDGAILVCSAADGMPMPQTREHI 120

Query: 121 LLSRQVGVP HIVVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP+I+VFLNK S Y+FPGDDTPIV GSA ALE  
 Sbjct: 121 LLARQVGVPYIIVFLNKCDSDDAELLELVEMEVRLLSKYDFPGDDTPIVKGSAKLAL 180

Query: 181 EAKAGNVGEWGEKVLKLM AE-VDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIER 239  
 G+ GE GE + +A+ +D+YITPER + FLMPVEDVFSI+GRGT VVTGR+ER  
 Sbjct: 181 ----GDTGELGEVAIMSLADALDYIPTPERAVDGAFLMPVEDVFSISGRGT VVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 G+VKG+G+E+ELVGT+ T KTT TGVEMFRK L++G+AGDNVG+LLRGTK+E+VERG VL  
 Sbjct: 237 GIVKVGEEIEIVGIKPTVKTCTGVEMFRKLLDQGGAGDNVGI LLRGTKREDVERGQVLA 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGRHTPFFTNYR PQFYVRTT DVTGSITLPEGVEMVMPG 359  
 KPGSITPH F E+YVLSK+EGGRHTPFF NYR PQFY RTTDTGSI LP+ EMVMPG  
 Sbjct: 297 KPGSITPHTFTAEVYVLSKDEGGRHTPFFNNYR PQFYFR TTDVTGSIELPKDKEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV ITV+LI+P+A+E G +FAIREGGRTVGAGVV+ I++  
 Sbjct: 357 DNVSITVKLI APIAMEEGLRFAIREGGRTVGAGVVAKILD 396

tr Q5HRK4 Translation elongation factor Tu [tuf] [Staphylococcus 394  
 Q5HRK4\_STAEQ epidermidis AA  
 (strain ATCC 35984 / RP62A)] align

Score = 560 bits (1444), Expect = e-158  
 Identities = 276/399 (69%), Positives = 320/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKF+R+ H NIGTIGHV HCKTTL+AAI+ VL+ G + YD IDNAP+EKERG  
 Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTTLTAAIATVLAKNGDTVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI T+HIEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGMPQTREHI  
 Sbjct: 61 ITINTAHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVP HIVVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSR VGVP +VVFLNK S Y+FPGDD P++AGSAL+ALE  
 Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDDEELLELVEMEVDRLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG 240  
 E+ +K+L IM VD YLPTPERD+K F+MPVEDVFSI GRGTV TGR+ERG  
 Sbjct: 181 -----GDAEYEQKILDLMQAVDDYIPTPERDSKPFMPVEDVFSITGRGT VATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LRG +E+V+RG VL  
 Sbjct: 236 QIKVGEEVEIIGMHETSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDEVQRGQVLAA 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360  
 PGSITPH KF+ E+YVLSK+EGGRHTPFFTNYRPQFY RTT DVTG + LPEG EMVMPGD  
 Sbjct: 296 PGSITPHTKFAEVYVLSKDEGGRHTPFFTNYRPQFYRTT DVTGVVNLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ I E  
 Sbjct: 356 NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIFE 394

sp Q9Z9L6 Elongation factor Tu (EF-Tu) [tuf] [Bacillus halodurans] 396 AA  
 EFTU\_BACHD align

Score = 560 bits (1443), Expect = e-158  
 Identities = 279/399 (69%), Positives = 323/399 (80%), Gaps = 7/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLK-GLAEMKDYNIDNAPQEKER 59  
 MAKEKF+R+ H NIGTIGHV HCKTTL+AAI+ VL+ + G YD ID AP+E+ER  
 Sbjct: 1 MAKEKFDRSKTHANIGTIGHVDHGKTTTLTAAITTVLAKRSGKGVAMAYDAIDGAPEERER 60

Query: 60 GITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREH 119  
 GITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGMPQTREH  
 Sbjct: 61 GITISTAHVEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREH 120

Query: 120 ILLSRQVGVP HIVVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRAL 179  
 ILLSRQVGVP++VVFLNK S Y+FPGDD P++ GSAL+AL

Sbjct: 121 ILLSRQVGVPYLVVFLNKCDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVIRGSALKAL 180

Query: 180 EEAKAGNVGEWGEKVLKMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239  
E EW EK+++LMA VD YIPTPERDTEK F+MPVEDVFSI GRGTV TGR+ER

Sbjct: 181 E-----GDAEWEEKIIEELMAAVDDYIPTPERDTEKPFMPVEDVFSITGRGTVATGRVER 235

Query: 240 GVVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298  
G + VGDEVEI+G+ +KTTVTGVEMFRK L+ EAGDN+G LLRG +EEV+RG VL

Sbjct: 236 GQLNVGDEVEIIGLEEEAKKTTVTGVEMFRKLLDYAEAGDNIGALLRGVSREEVQRGQVL 295

Query: 299 CKPGSITPHKKFEEIEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTGSIITLPEGVEMVMP 358  
KPG+ITPH F+ E+YVLSKEEGGRHTPEF+NYRQFY RTTDTG I LP+GVEMVMP

Sbjct: 296 AKPGTITPHTNFKAENVYVLSKEEGGRHTPFSSNYRPQFYFRTTDTGTIIQLPDGVEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 397  
GDNV++TVELI+P+A+E GTFK+IREGGRTVGAGVV++I

Sbjct: 356 GDNVEMTVELIAPIAIEEGTKFSIREGGRTVGAGVVASI 394

sp Q8NL22 Elongation factor Tu (EF-Tu) [tufA] [Xanthomonas 396  
EFTU\_XANAC axonopodis (pv. AA  
citri)] align

Score = 560 bits (1442), Expect = e-158  
Identities = 279/400 (69%), Positives = 325/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRNTNPVHNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
MAK KF RT PHVN+GTIGHV HGKTTL+AA++ + + + E K YD ID AP+EK RG

Sbjct: 1 MAKAKFERTKPHVNVGTIGHVDHGKTTLTAALTKEGAERFGGEFKAYDAIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAAGMPQTREHI 120  
ITL+T+H+EYE+ TRHYAHVDCPGHADYVKNMITGAAQMDGAILV SAAGMPQTREHI

Sbjct: 61 ITISTAHVEYESPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAAGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
LLSRQVGVPPIVVFINK S Y+FPGDDTPI+ GSA AL+

Sbjct: 121 LLSRQVGVPPIVFLNKADMVDDAEELLELVEMEVRLLSKYDFPGDDTPIIHGSARIALD 180

Query: 181 EAKAGNVGEWG-EKVLKMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239  
G+ + G +LKL+ +DS+IP P RD ++ FILMPVEDVFSI+GRGTVVTGRIER

Sbjct: 181 ----GDQSDIGVPAILKLVEALDSFIPEPTRDVRPFLMPVEDVFSISGRGTVVTGRIER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
G++KVGDE+EIVGIR TQKTTVTGVEMFRK L++G+AGDN G+LLRGTK+++VERG VLC

Sbjct: 237 GIIKVGDEIEIVGIRDITQKTTVTGVEMFRKLLDQGGAGDNAGLLLRGTRDDVERGQVLC 296

Query: 300 KPGSITPHKKFEEIEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTGSIITLPEGVEMVMPG 359  
KPGSI PH +FE E+YVLSK+EGGRHTPEF YRPQFY RTTD+TG+ LPEGVEMVMPG

Sbjct: 297 KPGSIKPHTFEAEVYVLSKDEGGRHTPFFKGYRPQFYFRTTDTGACQLPEGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
DNVK+ V LI+PVA++ G +FAIREGGRTVGAGVV+ II+

Sbjct: 357 DNVKMVVTLINPVAMDEGLRFAIREGGRTVGAGVVAKIIK 396

sp P33166 Elongation factor Tu (EF-Tu) (P-40) [tuf] [Bacillus 396  
EFTU\_BACSU subtilis] AA  
align

Score = 560 bits (1442), Expect = e-158  
Identities = 282/401 (70%), Positives = 320/401 (79%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLK-GLAEMKDYDNIDNAPQEKER 59  
MAKEKE+R+ H NIGTIGHV HGKTTL+AAI+ VL K G YD ID AP+E+ER  
Sbjct: 1 MAKEKFDRSKSHANIGTIGHVDHGKTTLTAAITTVLHKKSGKGTAMAYDQIDGAPEERER 60

Query: 60 GITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREH 119  
GITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREH  
Sbjct: 61 GITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREH 120

Query: 120 ILLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRAL 179  
ILLS+ VGVP+IVVFLNK 3 Y+FPGDD P+V GSAL+AL  
Sbjct: 121 ILLSKNVGVPYIVVFLNKCDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVVKGSALKAL 180

Query: 180 EEAKAGNVGEWGEKVLKILMAEVD SYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIER 239  
E EW K+ +LM VD YIPTPERDTEK F+MPVEDVFSI GRGTV TGR+ER  
Sbjct: 181 E-----GDAEWEAKIFELMDAVDEYIPTPERDTEKPFMPVEDVFSITGRGT VATGRVER 235

Query: 240 GVVKVGDEVEIVGIRA-TQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298  
G VVKVGDEVEI+G++ +KTTVTGVEMFRK L+ EAGDN+G LLRG +EE++RG VL  
Sbjct: 236 GQVKVGDEVEIIGLQREENKKT TTVTGVEMFRKLLDYAEAGDNIGALLRGVSREEIQRGQVL 295

Query: 299 CKPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMP 358  
KPG+ITPH KE+ E+YVLSKEEGGRHTPFF+NYRPQFY RTT DVTG I LPEGVEMVMP  
Sbjct: 296 AKPGTITPHSKFKA EYVLSKEEGGRHTPFFSNYRPQFYRTT DVTGIIHLPEGVEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
GDN ++ VELIS +A+E GT+F+IREGGRTVG+GVVS I E  
Sbjct: 356 GDNTEMNVELISTIAIEEGTRFSIREGGRTVGSGGVVSTITE 396

sp P64029 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus 394  
EFTU\_STAAW (strain AA  
MW2)] align

Score = 559 bits (1441), Expect = e-158  
Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
MAKEKE+R+ H NIGTIGHV HGKTTL+AAI+ VL+ G + + YD IDNAP+EKERG  
Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
ITI TSHIEY+T+ RHYAHVDCPGHADYVENMITGAAQMDG ILLVSAADGMPQTREHI  
Sbjct: 61 ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
LLSR VGVP +VVFLNK 3 Y+FPGDD P++AGSAL+ALE  
Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKILMAEVD SYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG 240  
++ EK+L+IM VD+YIPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG

Sbjct: 181 -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGT VATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL

Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360  
 PGSITPH +F+ E+YVLSK+EGGRHTPFF+NYRPQFY RTTDDVTG + LPEG EMVMPGD

Sbjct: 296 PGSITPHTEFKAENVYVLSKDEGGGRHTPFFSNYRPQFYFRTTDDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+

Sbjct: 356 NVENTVELIAPIAIEDGTRFSIREGGRTVGSGGVVTEIIK 394

sp Q6GBT9 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus] 394  
 EFTU\_STAAS (strain AA  
 MSSA476) ] align

Score = 559 bits (1441), Expect = e-158  
 Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAKEKF+R+ H NIGTIGHV HGKTTL+AAI+ VL+ G + + YD IDNAP+EKERG

Sbjct: 1 MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI TSHIEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG IIVVSAADGMPQTREHI

Sbjct: 61 ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LLSR VGVP +VVELNK S Y+FPGDD P++AGSAL+ALE

Sbjct: 121 LLSRNVGVPALVFLNKMVDMDDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTGRIERG 240  
 ++ EK+L+LM VD+YIPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG

Sbjct: 181 -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGT VATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 +KVG+EVEI+G+ T KTTVTGVEMFRK L+ EAGDN+G LLRG +E+V+RG VL

Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360  
 PGSITPH +F+ E+YVLSK+EGGRHTPFF+NYRPQFY RTTDDVTG + LPEG EMVMPGD

Sbjct: 296 PGSITPHTEFKAENVYVLSKDEGGGRHTPFFSNYRPQFYFRTTDDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+

Sbjct: 356 NVENTVELIAPIAIEDGTRFSIREGGRTVGSGGVVTEIIK 394

sp Q6GJC0 Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus] 394  
 EFTU\_STAAR (strain AA  
 MRSA252) ] align



Score = 559 bits (1441), Expect = e-158

Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
        MAKEKF+R+  H NIGTIGHV HGKTTL+AAI+ VL+  G +  + YD IDNAP+EKERG
Sbjct: 1  MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI TSHIEY+T+ RHYAHVDCPGHADVKNMITGAAQMDG ILVVSAADGMPQTREHI
Sbjct: 61  ITINTSHIEYQTDKRHYAHVDCPGHADVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LLSR VGVP +VVFINK                      S Y+FPGDD P++AGSAL+ALE
Sbjct: 121  LLSRNVGVPALVVFLNKVDMVDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
        ++ EK+L+LM VD+YIPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300
        +KVG+EVEL+G+ T KTTVTGVMFRK L+  EAGDN+G LLRG  +E+V+RG VL
Sbjct: 236  QIKVGEEVEIIGLHDTSKTTVTGVMFRKLLDYAEAGDNIGALLRGVAREDEVQRGQVLAA 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
        PGSITPH +P+ E+YVLSK+EGGRHTPFF+NYRPQFY RTTENVG + LPEG EMVMPGD
Sbjct: 296  PGSITPHTEFKAENVVLSKDEGGGRHTPFFSNYRPQFYFRTTDTVGVVHLPEGTEMVMPGD 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
        NV++VELI+P+A+E GT+F+IREGGRTVG+GVV+ II+
Sbjct: 356  NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

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sp  P99152      Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus 394
    EFTU_STAA  (strain AA
          N315)] align

```

Score = 559 bits (1441), Expect = e-158

Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
        MAKEKF+R+  H NIGTIGHV HGKTTL+AAI+ VL+  G +  + YD IDNAP+EKERG
Sbjct: 1  MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI TSHIEY+T+ RHYAHVDCPGHADVKNMITGAAQMDG ILVVSAADGMPQTREHI
Sbjct: 61  ITINTSHIEYQTDKRHYAHVDCPGHADVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LLSR VGVP +VVFINK                      S Y+FPGDD P++AGSAL+ALE
Sbjct: 121  LLSRNVGVPALVVFLNKVDMVDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
        ++ EK+L+LM VD+YIPTPERD++K F+MPVEDVEST GRGTV TGR+ERG
Sbjct: 181  -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300

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      +KVG+EVEI+G+  T KTTVTGVEMFRK L+  EAGDN+G LLRG  +E+V+RG VL
Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
      PGSITPH +F+ E+YVLSK+EGGRHTPFF+NYRPQFY RTTDDVTG + LPEG EMVMPGD
Sbjct: 296 PGSITPHTEFKAÉVYVLSKDEGGRHTPFFSNYPQFYFRTTDDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+
Sbjct: 356 NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

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sp P64028      Elongation factor Tu (EF-Tu) [tuf] [Staphylococcus aureus 394
EFTU_STAAM    (strain AA
Mu50 / ATCC 700699)] align

```

Score = 559 bits (1441), Expect = e-158  
Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRNTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAKEKF+R+  N NIGTIGHV HGKTTL+AAI+ VL+  G +  + YD IDNAP+EKERG
Sbjct: 1  MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI TSHIEY+T+ RHYAHVDCPGHADVKNMITGAAQMDG ILVVSADGMPQTREHI
Sbjct: 61  ITINTSHIEYQTDKRHYAHVDCPGHADVKNMITGAAQMDGGILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVP HIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LLSR VGVP +VFLNK S Y+FPGDD P++AGSAL+ALE
Sbjct: 121 LLSRNVGVPALVVFLNKVDMVDDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVD SYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      ++ EK+L+IM VD+YIPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181 -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGT VATGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +KVG+EVEI+G+  T KTTVTGVEMFRK L+  EAGDN+G LLRG  +E+V+RG VL
Sbjct: 236 QIKVGEEVEIIGLHDTSKTTVTGVEMFRKLLDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
      PGSITPH +F+ E+YVLSK+EGGRHTPFF+NYRPQFY RTTDDVTG + LPEG EMVMPGD
Sbjct: 296 PGSITPHTEFKAÉVYVLSKDEGGRHTPFFSNYPQFYFRTTDDVTGVVHLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      NV++TVELI+P+A+E GT+F+IREGGRTVG+GVV+ II+
Sbjct: 356 NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

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tr Q5HIC7      Translation elongation factor Tu [tuf] [Staphylococcus 394
Q5HIC7_STAAC  aureus AA
              (strain COL)] align

```

Score = 559 bits (1441), Expect = e-158  
Identities = 275/399 (68%), Positives = 324/399 (80%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MAKEKF+R+  H NIQTIGHV HGKTTL+AAI+ VL+  G +  + YD IDNAP+EKERG
Sbjct: 1  MAKEKFDRSKEHANIGTIGHVDHGKTTLTAAIATVLAKNGDSVAQSYDMIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI TSHIEY+T+ RHYAHVDCPGHADYVKNMITGAAQMDG ILLVSAADGMPQTREHI
Sbjct: 61  ITINTSHIEYQTDKRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LLSR VGVP +VVELNK                               S Y+FPGDD P++AGSAL+ALE
Sbjct: 121  LLSRNVGVPALVVFLNKVMDVDEELLELVEMEVRDLLSEYDFPGDDVPVIAGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
        .      ++ EK+L+LM  VD+YIPTPERD++K F+MPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  -----GDAQYEEKILELMEAVDTYIPTPERDSKPFMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVMERFKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300
        +KVG+EVEI+G+  T KTTVTGVMERK L+  EAGDN+G LLRG  +E+V+RG VL
Sbjct: 236  QIKVGEEVEIIGLHDTSKTTVTGVMERKLLDYAEAGDNIGALLRGVAREDVQRGQVLAA 295

Query: 301  PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVTSITLPEGVEMVMPGD 360
        PGSITPH +F+ E+YVLSK+EGGRHTPFET+NYRPQFY RTTDTVG + LPEG EMVMPGD
Sbjct: 296  PGSITPHTEFKAENVYVLSKDEGGRTPFSSNYRPQFYFRTTDTVGVVHLPEGTEMVMPGD 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
        NV++TVELI+P+A+E GR+F+IREGGRTVG+GVV+ II+
Sbjct: 356  NVENTVELIAPIAIEDGTRFSIREGGRTVGSGVVTEIIK 394

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tr Q5QWA3 Translation elongation factor EF-Tu [tufB\_1] [Idiomarina 394 AA  
Q5QWA3\_IDILO loihiensis]

align

Score = 559 bits (1441), Expect = e-158  
Identities = 271/399 (67%), Positives = 325/399 (80%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        M+KEKF R+ PHVN+GHTIGHV HGKTTL+AAI+ VL+  KD+ IDNAP+EKERG
Sbjct: 1  MSKEKFERSKPHVNVGTIGHVDHGKTTLTAAITTVLAKVYGGAAKDFAAIDNAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI+TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61  ITISTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
        LLSRQVGVP IVVF+NK                               S Y+FPGDD P++GSAL+ALE
Sbjct: 121  LLSRQVGVPFIVVFMNKCMDVDEELLELVEMEVRDLLSEYDFPGDDLPIVQGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
        +      EW +K+++L  +D+YIP PERD +K F+MP+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181  GDE-----EWSKKIVELADALDNYIPEPERDIDKPFIMPIEDVFSISGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVMERFKELEKGEAGDNVGVLLRGTKEEVERGMVLCK 300
        +V+ GDE EIVG++ T KTTVTGVMERK L++G AG+N+G LLRGTK+++VERG VL K
Sbjct: 236  IVRTGDECEIVGMKDTTKTTVTGVMERKLLDEGRAGENIGALLRGTKRDDVERGQVLAK 295

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Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360  
 FG+ITPH KFE E+YVLSK+EGGRHTPEE YRPQFY RTTDDVTG++ LPEGVEMVMPGD  
 Sbjct: 296 PGTITPHTKFEAEVYVLSKDEGGRHTPFFKGYRPQFYFRTTDDVTGAVELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 N+K V+LI+P+A++ G +FAIREGGRTVGAGVVS I++  
 Sbjct: 356 NLKFVVDLIAPIAMDEGLRFAIREGGRTVGAGVVSIMD 394

tr Q6N4Q4 Elongation factor Tu (EC 3.6.1.48) [tuf/ EF-Tu] 396  
 Q6N4Q4\_RHOPA [Rhodopseudomonas  
 palustris] AA  
align

Score = 558 bits (1439), Expect = e-158  
 Identities = 280/401 (69%), Positives = 323/401 (79%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF RT PH NIGTIGHV HGKT+L+AAI+ VL+ G A YD ID AP+EK RG  
 Sbjct: 1 MAKAKFERTKPHCNIGTIGHVDHGKTSLTAAITKVLAEETGATFTAYDQIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAAGMPQTREHI 120  
 ITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAAGMPQTREHI  
 Sbjct: 61 ITISTAHVEYETQNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAAGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP +VVFLNK S Y+FPGDD PIV GSAL ALE  
 Sbjct: 121 LLARQVGVPALVVFLNKCDMVDDPELLELVEMEVRELLSKYDFPGDDIPVKGSALE 180

Query: 181 --EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMPVEDVFSIAGRGTVVVTGRIE 238  
 +AK G+ + +L+LM +VD+YIP PER ++ FMPVEDVFSI+GRGTVVVTGR+E  
 Sbjct: 181 NSDAKLGH-----DAILELMRQVDAYIPQPERPIDQPFLMPVEDVFSISGRGTVVVTGRVE 235

Query: 239 RGVVKGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298  
 RG++KVGDE+EIVGIR TQKTT TGVEMFRK L++G+AGDN+G LLRGTK+E+VERG VL  
 Sbjct: 236 RGILKVGDEIEIVGIRDQKTTCTGVEMFRKLLDQAGDNIGALLRGTKREDVERGQVL 295

Query: 299 CKPGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMP 358  
 CKPGS+ PH KF+ E Y+L+KEEGGRHTPFFFTNYRPQFY RTTDDVTG + LPEG EMVMP  
 Sbjct: 296 CKPGSVKPHTKFAEAYILTKEEGGRHTPFFFTNYRPQFYFRTTDDVTGVVHLPEGTEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 GDN+ + V LI P+A+E +FAIREGGRTVGAGVV+ IIE  
 Sbjct: 356 GDNIAEVHLIVPIAMEEKLRFIREGGRTVGAGVVAIIE 396

tr Q73F98 Translation elongation factor Tu [tuf] [Bacillus cereus] 395  
 Q73F98\_BACC1 (strain  
 ATCC 10987) ] AA  
align

Score = 558 bits (1439), Expect = e-158  
 Identities = 275/400 (68%), Positives = 322/400 (79%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ G AE + YD ID AP+E+ERG  
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITTVLAKAGGAEEARGYDQIDAAPEERERG 60

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Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGMPQTREHI
Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+IVVFLNK S Y FPGDD P++ GSAL+AL+
Sbjct: 121 LLSRQVGVPYIVVFLNKCDMVDDEELLELVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      +W K+++LMAEVD+YIPTPER+P+K FILMPVEDVFSI GRGTV TGR+ERG
Sbjct: 181 -----GEADWEAKIIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      +VKVGD VEI+G+ TTVTGVEMFRK L++ +AGDN+G LARG +E+++RG VL
Sbjct: 236 IVKVGDVVEIIGLAEENASTTVTGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300 KPGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
      K GS+ H KF+ E++VLSKEEGGRHTPEF NYRPQFY RTTDTG I LPEG EMVMPG
Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDTGTIIQLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      DNV++T+ELI+P+A+E GTKF+IREGGRTVG GVV+ I+E
Sbjct: 356 DNVENTIELIPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

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sp Q814C4      Elongation factor Tu (EF-Tu) [tuf] [Bacillus cereus] 395
EFTU_BACCR (strain ATCC AA
14579 / DSM 31)] align

```

Score = 558 bits (1438), Expect = e-158  
 Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

```

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      MAK KF R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ G AE + YD ID AP+E+ERG
Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITTVLAKAGGAEEARGYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDG ILVVSAADGMPQTREHI
Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LLSRQVGVP+IVVFLNK S Y FPGDD P++ GSAL+AL+
Sbjct: 121 LLSRQVGVPYIVVFLNKCDMVDDEELLELVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
      +W K+++LMAEVD+YIPTPER+P+K FILMPVEDVFSI GRGTV TGR+ERG
Sbjct: 181 -----GEADWEAKIIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
      +VKVGD VEI+G+ TTVTGVEMFRK L++ +AGDN+G LARG +E+++RG VL
Sbjct: 236 IVKVGDVVEIIGLAEENASTTVTGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300 KPGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359
      K GS+ H KF+ E++VLSKEEGGRHTPEF NYRPQFY RTTDTG I LPEG EMVMPG
Sbjct: 296 KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDTGTIIQLPEGTEMVMPG 355

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Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DN+++T+ELL+P+A+E GTKF+IREGGRTVG GVV+ I+E  
 Sbjct: 356 DNIEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

sp Q81VT2 Elongation factor Tu (EF-Tu) [tuf] [Bacillus anthracis] 395 AA  
 EFTU\_BACAN

align

Score = 558 bits (1438), Expect = e-158  
 Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAK KF R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ G AE + YD ID AP+E+ERG  
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITTVLAKAGGAEEARGYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI+T+H+EYETETRHYAHVDCPGHADYVKNMITGAAQMDG ILVVSADGMPQTREHI  
 Sbjct: 61 ITISTAHVEYETETRHYAHVDCPGHADYVKNMITGAAQMDGGILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP+IVVFLNK S Y FPGDD P++ GSAL+AL+  
 Sbjct: 121 LLSRQVGVPPIVFLNKCDMVDDEELLELVEMEVRLDSEYGFPGDDIPVIKGSALKALQ 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFIMPVEDVFSIAGRGTVTGRIERG 240  
 +W K+++LMAEVD+YIPTPER+T+K FIMPVEDVFSI GRGTV TGR+ERG  
 Sbjct: 181 -----GEADWEAKIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241 VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 +VVKVG VEL+G+ TTVTGVEMFRK L++ +AGDN+G LLRG +E+++RG VL  
 Sbjct: 236 IVKVGDVVEIIGLAEENASTTVTGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPG 359  
 K GS+ H KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTDTG I LPEG EMVMPG  
 Sbjct: 296 KSGSVKAHAKFKAIEVFLVLSKEEGGRHTPFFANYRPQFYRTTDTGTIIQLPEGTEMVMPG 355

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DN+++T+ELL+P+A+E GTKF+IREGGRTVG GVV+ I+E  
 Sbjct: 356 DNIEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

tr Q6HPR0 Protein-synthesizing GTPase (Translation elongation 395  
 Q6HPR0\_BACHK factor Tu AA  
 (EF-TU)) (EC 3.6.5.3) [tufA] [Bacillus thuringiensis  
 (subsp. konkukian)] align

Score = 558 bits (1438), Expect = e-158  
 Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAK KF R+ PHVNIGTIGHV HGKTTL+AAI+ VL+ G AE + YD ID AP+E+ERG  
 Sbjct: 1 MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITTVLAKAGGAEEARGYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

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                ITI+T+H+EYETETRHYAHVDCPGHADVKNMITGAAQMDG ILLVSAADGMPQTREHI
Sbjct: 61  ITISTAHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
                LLSRQVGVP+IVVFLNK                               S Y FPGDD P++ GSAL+AL+
Sbjct: 121  LLSRQVGVPPIVFLNKCDMVDDEELLELVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
                +W K+++LMAEVD+YIPTPER+T+K FILMPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  -----GEADWEAKIIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
                +VVKVG D VEI+G+          TTVTGVEMFRK L++ +AGDN+G LLRG +E+++RG VL
Sbjct: 236  IVKVGDVVEIIGLAEENASTTVTGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300  KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPG 359
                K GS+ H KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTDDVTG I LPEG EMVMPG
Sbjct: 296  KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDDVTGIIQLPEGTEMVMPG 355

Query: 360  DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
                DN+++T+ELL+P+A+E GTEK+IREGGRTVG GVV+ I+E
Sbjct: 356  DNIEMTIELIPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

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tr Q63H92      Protein-synthesizing GTPase (Translation elongation      395
Q63H92_BACCZ factor Tu                                         AA
                (EF-TU)) (EC 3.6.5.3) [tufA] [Bacillus cereus (strain align
                2K) ]

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Score = 558 bits (1438), Expect = e-158

Identities = 274/400 (68%), Positives = 322/400 (80%), Gaps = 6/400 (1%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
                MAK KF R+ PHVNIGTIGHV HGKTTL+AAAL+ VL+ G AE + YD ID AP+E+ERG
Sbjct: 1  MAKAKFERSKPHVNIGTIGHVDHGKTTLTAAITTVLAKAGGAEGARYDQIDAAPPEERERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
                ITI+T+H+EYETETRHYAHVDCPGHADVKNMITGAAQMDG ILLVSAADGMPQTREHI
Sbjct: 61  ITISTAHVEYETETRHYAHVDCPGHADVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
                LLSRQVGVP+IVVFLNK                               S Y FPGDD P++ GSAL+AL+
Sbjct: 121  LLSRQVGVPPIVFLNKCDMVDDEELLELVEMEVRDLLSEYGFPGDDIPVIKGSALKALQ 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
                +W K+++LMAEVD+YIPTPER+T+K FILMPVEDVFSI GRGTV TGR+ERG
Sbjct: 181  -----GEADWEAKIIELMAEVDAYIPTPERETDKPFLMPVEDVFSITGRGTVATGRVERG 235

Query: 241  VVKVGDEVEIVGI-RATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
                +VVKVG D VEI+G+          TTVTGVEMFRK L++ +AGDN+G LLRG +E+++RG VL
Sbjct: 236  IVKVGDVVEIIGLAEENASTTVTGVEMFRKLLDQAQAGDNIGALLRGVAREDIQRGQVLA 295

Query: 300  KPGSITPHKKFEEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPG 359
                K GS+ H KF+ E++VLSKEEGGRHTPFF NYRPQFY RTTDDVTG I LPEG EMVMPG
Sbjct: 296  KSGSVKAHAKFKAEVFVLSKEEGGRHTPFFANYRPQFYFRTTDDVTGIIQLPEGTEMVMPG 355

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Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DN+++T+ELL+P+A+E GTKF+IREGGRTVG GVV+ I+E  
 Sbjct: 356 DNIEMTIELIAPIAIEEGTKFSIREGGRTVGYGVVATIVE 395

tr Q6MJ00 Translation elongation factor Tu (EC 3.6.1.48) [tuf] 396  
 Q6MJ00\_BDEBA [Bdellovibrio 396  
 bacteriovorus] align

Score = 557 bits (1436), Expect = e-157  
 Identities = 275/400 (68%), Positives = 321/400 (79%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 M+KEKE R PHVNIGTIGHV HGKTTL+AAI+ L+ G A+ YD ID +P+EK RG  
 Sbjct: 1 MSKEKFTRNKPHVNIGTIGHVDHGKTTLTAAITTTLAASGKAQAMAYDQIDKSPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI+T+H+EYET+ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVS+ADGMPQTREHI  
 Sbjct: 61 ITISTTHVEYETDNRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP +VVF+NK S YEFPGDD P+V GSAL+ALE  
 Sbjct: 121 LLARQVGVPALVVFMMNKVDMVDDKELLELELVRELLSKYEFPGDDIPVVKGSALKALE 180

Query: 181 EAKAGNVGEWGEK-VLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIER 239  
 G+ E G ++KLM D+YIP F R +KTFMLPVEDVFSI+GRGTVVTGR+ER  
 Sbjct: 181 ----GDTSEIGRPAIMKLMEACDTYIPAPVRAVDKTFMLPVEDVFSISGRGTVVTGRVER 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 G+VKVGDE+ELVGIR TQKTTVTG+EMERK L++G+AGDN GVLIRGTTKEE+VERG VL  
 Sbjct: 237 GIVKVGDEIEIVGIRPTQKTTVTGIEMFRKLLDEGQAGDNCVLLRGTKKEDVERGQVLV 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPOFYVRTTDTGTSITLPEGVEMVMPG 359  
 KPG++ PHKKF+ E Y+L+KEEGGRHTPFF YRPFY RTTDTG TL G EMVMPG  
 Sbjct: 297 KPGTVKPHKKFKAAYILTKEEGGRHTPFFNGYRPOFYFRTTDTGVTCTLKAGTEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 D ++++VELI+P+A+E +FAIREGGRTVGAGVV+ I+E  
 Sbjct: 357 DKIEVSVELIAPIAIEEKELRFAIREGGRTVGAGVVTEILE 396

tr Q9F9S8 Eftu [eftu] [EDTA-degrading bacterium 391 AA  
 Q9F9S8\_9PROT BNC1] align

Score = 557 bits (1435), Expect = e-157  
 Identities = 284/399 (71%), Positives = 320/399 (80%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF RT PHVNIGTIGHV HGKT+L+AAI+ K E K YD ID AP+EK RG  
 Sbjct: 1 MAKGKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEEKARG 55

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI+T+H+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 56 ITISTAHVEYETENRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 115



Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP I VFLNK S YEFPGDD PIV GSAL ALE  
 Sbjct: 116 LLARQVGVPPIVFLNKVDQVDDPELLELVELEIRELLSKYEFPGDDIPIVKGSALAAL 175

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240  
 ++ +GE + V +LMAEVD YIPTER ++ FIMP+EDVFSI+GRGTVVTGR+ERG  
 Sbjct: 176 DSNK-EIGE--DAVRQLMAEVDKYIPTPERPIDQPFLMPIEDVFSISGRGTVVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 VVKVG+EVEIVGIR T KTTVTGVEMFRK L++G+AGDN+G LLRG +E VERG VL K  
 Sbjct: 233 VVKVGEEVEIVGIRPTSKT TTVTGVMFRKLLDQGGAGDNIGALLRGIDREGVERGQVLAK 292

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360  
 PGS+TPH KF+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTDTVG +TLPEG EMVMPGD  
 Sbjct: 293 PGSVTPHTKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTTDTGVVTLPEGTEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NV + V LI P+A+E +FAIREGGRTVGAG+V++I E  
 Sbjct: 353 NVTMDVTLIVPIAMEERLRFAIREGGRTVGAGIVASITE 391

tr Q5PIW4 Elongation factor Tu [tufA] [Salmonella paratyphi-a] 394 AA  
 Q5PIW4\_SALPA

align

Score = 556 bits (1434), Expect = e-157

Identities = 272/398 (68%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 M+KEKE RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG  
 Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120  
 ITI TSH+EY+T TRHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGMPQOTREHI  
 Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGMPQOTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LL: RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE  
 Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240  
 EW K++L +DSYIP PER +K EL+P+EDVEST+GRGTVVTGR+ERG  
 Sbjct: 181 -----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 ++KVG+EVEIVGI+ TQK+T TGVMFRK L++G AG+NVGVLLRG K+EE+ERG VL K  
 Sbjct: 236 IIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360  
 PG+I PH KFE E+Y+LSK+EGGRHTPEE YRPQFY RTTDTVG+I LPEGVEMVMPGD  
 Sbjct: 296 PGTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398  
 N+K+ V LI P+A++ G +FAIREGGRTVGAGV++ ++  
 Sbjct: 356 NIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVAKVL 393

tr Q57H76 Protein chain elongation factor EF-Tu (Duplicate of 394  
 Q57H76\_SALCH tufA) [tufB] AA  
 [Salmonella cholerae-suis (Salmonella enterica)] align

Score = 556 bits (1434), Expect = e-157  
 Identities = 272/398 (68%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 M+KEKEF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG  
 Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI TSH+EY+T TRHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGMPQTREHI  
 Sbjct: 61 ITINTSHVEYDTPTRHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE  
 Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVD SYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240  
 EW K++L +DSYIP PER +K FL+P+EDVFSI+GRGT VVTGR+ERG  
 Sbjct: 181 -----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGT VVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 ++KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL K  
 Sbjct: 236 IIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAK 295

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360  
 PG+I PH KFE E+Y+LSK+EGGRHTPF YRPQFY RTT DVTG+I LPEGVEMVMPGD  
 Sbjct: 296 PGTIKPHTKFESEVYILSKDEGGRHTPF FKG YRPQFYRTT DVTGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398  
 N+K+ V LI P+A++ G +FAIREGGRTVGAGV+ ++  
 Sbjct: 356 NIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 393

tr Q6N0C2 EF-Tu [orf3309] [Magnetospirillum 396 AA  
 Q6N0C2\_9PROT gryphiswaldense] align

Score = 556 bits (1434), Expect = e-157  
 Identities = 280/399 (70%), Positives = 319/399 (79%), Gaps = 3/399 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF R PH NIGTIGHV HGKT+L+AAI+ VL+ G A YD ID AP+EK RG  
 Sbjct: 1 MAKAKFERNKPHCNIGTIGHVDHGKTSLTAAITKVLAETGGATFTAYDQIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI+T+H+EYET PHYAHVDCPGHADVKNMITGAAQMDG I LVVSAADGMPQTREHI  
 Sbjct: 61 ITISTAHVEYETANRHYAHVDCPGHADVKNMITGAAQMDGGILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP +VVF+NK S+Y+FPGDD PIV GSAL ALE  
 Sbjct: 121 LLARQVGVPALVVF MNKCDMVDDELLDLVELEVRELLSSYDFPGDDIPIVRSALCALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVD SYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240

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      + K  +G  + +L LMAEVD YIP PER  +K FIMP+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181 D-KQPEIGR--DAILALMAEVDKYIPQPERPKDKPFLMPIEDVFSISGRGTVVTGRVERG 237

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      VVKVG+EVEIVGI+ T KTF TGVEMFRK L++GEAGDN+G LLRG K+E+VERG VL
Sbjct: 238 VVKVGEEVEIVGIKPTVKTCTGVEMFRKLLDQGEAGDNIGALLRGVKREDVERGQVLAA 297

Query: 301 PGSITPHKKFEEEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
      PGSITPH KF E Y+L+KEEGGRHTPFFFTNYRPQFY RTTDDVTG + LPEG EMVMPGD
Sbjct: 298 PGSITPHTKFTAAYIILNKEEGGRHTPFFFTNYRPQFYFRTTDDVTGMVYLPEGTEMVMPGD 357

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      NV +TV+LL+P+A++ G +FAIREGGRTVGAGVV+ IIE
Sbjct: 358 NVSMTVQLIAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

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sp P26184      Elongation factor Tu (EF-Tu) [tuf] [Flexistipes      396
  EFTU_FLESI  sinusarabici]                                     AA
                                                                align

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Score = 556 bits (1433), Expect = e-157  
 Identities = 275/399 (68%), Positives = 325/399 (80%), Gaps = 3/399 (0%)

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Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
      M+K+K+ R PHVN+GTHGV HOKTTL+AA++ VLSLKG A+ ++ NID AP+EKERG
Sbjct: 1  MSKQKYERKKPHVNVGTIGHVDHGKTTLTAAATHVLSLKGYADYIEFGNIDKAPEEKERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITIAT+H+EYE++ RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI
Sbjct: 61  ITIATAHVEYESDKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP IVVF+NK + YEFPGDD PI+ GSAL+ALE
Sbjct: 121  LLARQVGVPISIVFMNKCMDVDEELLELEIRDLLNTYEFPGDDIPIKGSALQALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFIMPVEDVFSIAGRGTVVTGRIERG 240
      A+ E + + +L+ +D YTP PERD +K FIMP+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181  NAEDE---EKTCKIWELLQAMDDYIPAPERDIDKPFILMPIEDVFSISGRGTVVTGRVERG 237

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      V+V DE+RIVG+ T+KT VTGVEMFRK L++GEAGDNVGVLLRG KK++VERG VL K
Sbjct: 238  KVRVQDEIEIVGLTDTRKTVVTGVEMFRKILDEGEAGDNVGVLLRGIKKDDVERGQVLAK 297

Query: 301  PGSITPHKKFEEEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDDVTGSITLPEGVEMVMPGD 360
      PGSITPH+KE+ E Y+L+KEEGGRHTPFF+ YRPQFY RTTDDVTG ITL EGVEVEMVMPGD
Sbjct: 298  PGSITPHRKFKCEAYILTKEEGGRHTPFFSGYRPQFYFRTTDDVTGVITLAEGVEMVMPGD 357

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
      N+ V+LI P+A+E G +FAIREGGRTVGAGVV+ I+E
Sbjct: 358  NISCDVDLIQPIAMEQGLRFAIREGGRTVGAGVVTEIVE 396

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sp Q83JC4      Elongation factor Tu (EF-Tu) [tufA] [Shigella flexneri] 393 AA
  EFTU_SHIFL                                         align

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Score = 555 bits (1431), Expect = e-157

Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

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Query: 2  AKEKFNRNTPHVNIGTIGHVHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI 61
      +KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+      + +D IDNAP+EK RGI
Sbjct: 1  SKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI 60

Query: 62  TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHIL 121
      TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQTREHIL
Sbjct: 61  TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPQTREHIL 120

Query: 122  LSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 181
      L RQVGVP+I+VFLNK      S Y+FPGDDTPIV GSAL+ALE
Sbjct: 121  LGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVGRSALKALE- 179

Query: 182  AKAGNVGEWGEKVLKMAEVD SYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG V 241
      EW K+L+L +DSYIP PER +K FL+P+EDVFSI+GRGT VVTGR+ERG+
Sbjct: 180  ----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGT VVTGRVERGI 235

Query: 242  VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301
      +KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL KP
Sbjct: 236  IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENGVLLRGIKREEIERGQVLAKP 295

Query: 302  GSITPHKKFEEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGDN 361
      G+I PH KPE E+Y+LSK+EGGRHTPFF YRPQFY RTT DVTG+I LPEGVEMVMPGDN
Sbjct: 296  GTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTT DVTGTIELPEGVEMVMPGDN 355

Query: 362  VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      +K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
Sbjct: 356  IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

```

```

sp POA6N1      Elongation factor Tu (EF-Tu) (P-43) [tufA] [Escherichia      393
  EFTU_ECOLI coli]
                                           AA
                                           align

```

Score = 555 bits (1431), Expect = e-157

Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

```

Query: 2  AKEKFNRNTPHVNIGTIGHVHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI 61
      +KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+      + +D IDNAP+EK RGI
Sbjct: 1  SKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI 60

Query: 62  TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPQTREHIL 121
      TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQTREHIL
Sbjct: 61  TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPQTREHIL 120

Query: 122  LSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 181
      L RQVGVP+I+VFLNK      S Y+FPGDDTPIV GSAL+ALE
Sbjct: 121  LGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVGRSALKALE- 179

Query: 182  AKAGNVGEWGEKVLKMAEVD SYIPTPERDTEKTFILMPVEDVFSIAGRGT VVTGRIERG V 241
      EW K+L+L +DSYIP PER +K FL+P+EDVFSI+GRGT VVTGR+ERG+
Sbjct: 180  ----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGT VVTGRVERGI 235

Query: 242  VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301

```

```

      +KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLRLG K+EE+ERG VL KP
Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPOFYVRTTDTGSIITLPEGVEMVMPGDN 361
      G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDTG+I LPEGVEMVMPGDN
Sbjct: 296 GTIKPHTKFESVYILSKDEGGRHTPFFKGYRPOFYFRTTDTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      +K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
Sbjct: 356 IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

```

```

sp P0A6N2      Elongation factor Tu (EF-Tu) (P-43) [tufA] [Escherichia      393
  EFTU_ECOL6 coli 06] AA
                                align

```

Score = 555 bits (1431), Expect = e-157  
 Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

```

Query: 2  AKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI 61
      +KEKE RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RGT
Sbjct: 1  SKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI 60

Query: 62  TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHIL 121
      TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHIL
Sbjct: 61  TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHIL 120

Query: 122 LSRQVGVPVHIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 181
      L RQVGVP+I+VFLNK S Y+FPGDTPIV GSAL+ALE
Sbjct: 121 LGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRILLSQYDFPGDDTPIVRGSALKALE- 179

Query: 182 AKAGNVGEWGEKVLKMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 241
      EW K+L+L +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG+
Sbjct: 180 ----GDAEWEAKILELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKEEVERGMVLCKP 301
      +KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLRLG K+EE+ERG VL KP
Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPOFYVRTTDTGSIITLPEGVEMVMPGDN 361
      G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDTG+I LPEGVEMVMPGDN
Sbjct: 296 GTIKPHTKFESVYILSKDEGGRHTPFFKGYRPOFYFRTTDTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      +K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
Sbjct: 356 IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

```

```

sp P0A6N3      Elongation factor Tu (EF-Tu) (P-43) [tufA] [Escherichia      393
  EFTU_ECO57 coli
                                0157:H7] AA
                                align

```

Score = 555 bits (1431), Expect = e-157  
 Identities = 272/397 (68%), Positives = 319/397 (79%), Gaps = 5/397 (1%)

```

Query: 2  AKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI 61
+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RGI
Sbjct: 1  SKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI 60

Query: 62  TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREHIL 121
TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPMPQTREHIL
Sbjct: 61  TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGMPMPQTREHIL 120

Query: 122  LSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 181
L RQVGVP+I+VELNK S Y+FPGDDTPIV GSAL+ALE
Sbjct: 121  LGRQVGVPYIIVFLNCKMVDDEELLELVEMEVRLLSQYDFPGDDTPIVGRSALKALE- 179

Query: 182  AKAGNVGEWGEKVLKMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 241
EW K+L+L +DSYIP PER +K FL+P+EDVFSI+GRGTVVTGR+ERG+
Sbjct: 180  ----GDAWEAKILELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVTGRVERGI 235

Query: 242  VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301
+KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL KP
Sbjct: 236  IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLA KP 295

Query: 302  GSITPHKKFEEIYVLSKEEGGRHTPFFTNYPQFYVRTTDTGSIITLPEGVEMVMPGDN 361
G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDTVTG+I LPEGVEMVMPGDN
Sbjct: 296  GTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPFYFRTTDTGTIELPEGVEMVMPGDN 355

Query: 362  VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
Sbjct: 356  IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

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```

tr Q5ZYP5 Translation elongation factor Tu (EF-Tu) (EC 3.6.5.3) 396
Q5ZYP5_LEGPH [tufB] AA
[Legionella pneumophila subsp. pneumophila (strain align
Philadelphia 1 / ATCC 33152)]

```

Score = 555 bits (1430), Expect = e-157  
Identities = 278/400 (69%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI 60
MAKEKF R PHVN+GTIGHV HGKTTL+AAI+ +++ K K YD ID AP+E+ERG
Sbjct: 1  MAKEKFERKKPHVNVGTIGHVDHGKTTLTAAITTIMAKKYGGTAKAYDQIDAAPEERERG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120
ITI+T+H+EYE+ +RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREHI
Sbjct: 61  ITISTAHVEYESASRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALEE 180
LLSRQVGVP+IVVF+NK S+Y+FPGDD PIV GSAL+ALE
Sbjct: 121  LLSRQVGVPYIIVFMNKADMVDDPELLELVEMEVRDLLSSYDFPGDDIPIVGSALKALE 180

Query: 181  EAKAGNVGEWGEKVL-KLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIER 239
G + G K + KL+ +DSYIP R R+ +K FL+P+EDVFSI+GRGTVVTGR+E
Sbjct: 181  ----GEDSDIGVKAIEKLVETMSYIPEPVRNIDKPFLLPIEDVFSISGRGTVVTGRVES 236

Query: 240  GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299
G+VKVG+EVEIVGIR TQKTT TGVEMFRK L++G AGDNVGVLLRGTK+EEVERG VL
Sbjct: 237  GIVKVGEEVEIVGIRDITQKTTCTGVEMFRKLLDEGRAGDNVGVLLRGTKRDEVERGQVLA 296

```

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359  
 KPG+I PH KFE E+YVLSKEEGGRHTEFF. YRFQFY RTTDTVGT+ LP GVEMVMPG  
 Sbjct: 297 KPGTIKPHTKFEAEVYVLSKEEGGRHTPFFNGYRPQFYFRTTDTVGTCDLPSGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV++ V L +P+A++ G +FAIREGGRTVGAGVV+ IIE  
 Sbjct: 357 DNVQLVVS LHAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

tr Q5X873 Translation elongation factor Tu [tufA] [Legionella 396  
 Q5X873\_LEGPA. *pneumophila* AA  
 (strain Paris)] align

Score = 555 bits (1430), Expect = e-157  
 Identities = 278/400 (69%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAKEKF R PHVN+GTIGHV HGKTTL+AAI+ +++ K K YD ID AP+E+ERG  
 Sbjct: 1 MAKEKFERKKPHVNVGTIGHVDHGKTTLTAAITTIMAKKYGGTAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI+T+H+EYE+ +RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 61 ITISTAHVEYESASRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVVFNLKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP+IVVF+NK S+Y+FPGDD PIV GSAL+ALE  
 Sbjct: 121 LLSRQVGVPYIVVF MNKADMVDDPELLELVEMEVRDLLSSYDFPGDDIPIVVGSALKALE 180

Query: 181 EAKAGNVGEWGEKVL-KLMAEVD SYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTGRIER 239  
 G + G K + KL+ +DSYIP P R+ +K FL+P+EDVFSI+GRGT VVTGR+E  
 Sbjct: 181 ----GEDSDIGVKAIEKLVETMSYIPEPVRNIDKPFLLPIEDVFSISGRGT VVTGRVES 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 G+VKVG+EVEIVGIR TQKTT TGVEMFRK L++G AGDNVGVLLRGTK++EVERG VL  
 Sbjct: 237 GIVKVGEEVEIVGIRDTQKTTCTGVEMFRKLLDEGRAGDNVGVLLRGTKRDEVERGQVLA 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPG 359  
 KPG+I PH KFE E+YVLSKEEGGRHTEFF YRFQFY RTTDTVGT+ LP GVEMVMPG  
 Sbjct: 297 KPGTIKPHTKFEAEVYVLSKEEGGRHTPFFNGYRPQFYFRTTDTVGTCDLPSGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV++ V L +P+A++ G +FAIREGGRTVGAGVV+ IIE  
 Sbjct: 357 DNVQLVVS LHAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

tr Q57J27 Protein chain elongation factor EF-Tu (Duplicate of 409  
 Q57J27\_SALCH tufA) [tufB] AA  
 [Salmonella cholerae-suis (Salmonella enterica)] align

Score = 555 bits (1430), Expect = e-157  
 Identities = 271/398 (68%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 ++KEKE RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RG

```

Sbjct: 16 VSKEKFERTKPHVNVGTIGHVDHGKTTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARG 75

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQOTREHI 120
      ITI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQOTREHI
Sbjct: 76 ITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQOTREHI 135

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
Sbjct: 136 LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRSALKALE 195

Query: 181 EAKAGNVGEWGEKVLKILMAEVD SYIPTPERDTEKTFIMPVEDVFSIAGRGT VVTGRIERG 240
      EW K+++L +DSYIP PER +K FL+P+EDVESI+GRGT VVTGR+ERG
Sbjct: 196 -----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGT VVTGRVERG 250

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      ++KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL K
Sbjct: 251 IIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAK 310

Query: 301 PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360
      PG+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTT DVTG+I LPEGVEMVMPGD
Sbjct: 311 PGTIKPHTKFESEVYILSKDEGGRHTPFFFKGYRPQFYRTT DVTGTIELPEGVEMVMPGD 370

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      N+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++
Sbjct: 371 NIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 408

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sp " POA1H5      Elongation factor Tu (EF-Tu) [tufA] [Salmonella      393
    EFTU_SALTY typhimurium]                                     AA
                                                                align

```

Score = 555 bits (1429), Expect = e-157  
 Identities = 271/397 (68%), Positives = 319/397 (80%), Gaps = 5/397 (1%)

```

Query: 2 AKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERGI 61
      +KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RGI
Sbjct: 1 SKEKFERTKPHVNVGTIGHVDHGKTTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI 60

Query: 62 TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSADGMPQOTREHIL 121
      TI TSH+EY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGMPQOTREHIL
Sbjct: 61 TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQOTREHIL 120

Query: 122 LSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALEE 181
      L RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE
Sbjct: 121 LGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRSALKALE- 179

Query: 182 AKAGNVGEWGEKVLKILMAEVD SYIPTPERDTEKTFIMPVEDVFSIAGRGT VVTGRIERG 241
      EW K+++L +DSYIP PER +K FL+P+EDVESI+GRGT VVTGR+ERG+
Sbjct: 180 ----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGT VVTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301
      +KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL KP
Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGDN 361
      G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTT DVTG+I LPEGVEMVMPGDN

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Sbjct: 296 GTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398

+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++

Sbjct: 356 IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

sp POA1H6 Elongation factor Tu (EF-Tu) [tufA] [Salmonella typhi] 393 AA  
EFTU\_SALT1

align

Score = 555 bits (1429), Expect = e-157

Identities = 271/397 (68%), Positives = 319/397 (80%), Gaps = 5/397 (1%)

Query: 2 AKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERGI 61  
+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IDNAP+EK RGI

Sbjct: 1 SKEKFERTKPHVNVGTIGHVDHGKTTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGI 60

Query: 62 TIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHIL 121  
TI TSH+AY+T TRHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHIL

Sbjct: 61 TINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHIL 120

Query: 122 LSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXAYEFPGDDTPIVAGSALRALEE 181  
L RQVGVP+I+VFLNK S Y+FPGDDTPIV GSAL+ALE

Sbjct: 121 LGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRSALKALE- 179

Query: 182 AKAGNVGEWGEKVLKMAEVDYSIPTPERDTEKTFILMPVEDVFSIAGRGTVVGTGRIERG 241  
EW K+++L +DSYIP PER +K FL+P+EDVFSI+GRGTVVGTGR+ERG+

Sbjct: 180 ----GDAEWEAKIIELAGFLDSYIPEPERAIDKPFLLPIEDVFSISGRGTVVGTGRVERGI 235

Query: 242 VKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKP 301  
+KVG+EVEIVGI+ TQK+T TGVEMFRK L++G AG+NVGVLLRG K+EE+ERG VL KP

Sbjct: 236 IKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENGVLLRGIKREEIERGQVLAKP 295

Query: 302 GSITPHKKFEEIYVLSKEEGGRHTPFFFTNYRPOFYFVRTTDDVTGSITLPEGVEMVMPGDN 361  
G+I PH KFE E+Y+LSK+EGGRHTPFF YRPQFY RTTDDVTG+I LPEGVEMVMPGDN

Sbjct: 296 GTIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDDVTGTIELPEGVEMVMPGDN 355

Query: 362 VKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398

+K+ V LI P+A++ G +FAIREGGRTVGAGVV+ ++

Sbjct: 356 IKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVL 392

sp O31298 Elongation factor Tu (EF-Tu) [tuf] [Buchnera aphidicola] 394  
EFTU\_BUCAP (subsp. AA

Schizaphis graminum)]

align

Score = 555 bits (1429), Expect = e-157

Identities = 272/398 (68%), Positives = 318/398 (79%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
M+KEKF R PH+N+GTIGHV HGKTTL+AAI+ VLS K + +D IDNAP+EK RG

Sbjct: 1 MSKEKFQRVKPHINVGTIGHVDHGKTTTLTAAITTVLSKKYGGSSARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

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      ITI TSH+FY+TE RYAHVDCPGHADY+KNMITGAAQMDGAILVV+A DGMPQTREHI
Sbjct: 61 ITINTSHVEYDTELRYAHVDCPGHADYIKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL RQVGVP+I+VFLNK + Y+FPGDDTPI+ GSAL+ALE
Sbjct: 121 LLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVDRDLLTQYDFPGDDTPIIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      +W K+L L +D+YIP P+R ++ FL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 181 -----GDADWESKILDLSKFLDITYIPEPKRAIDQPFLLPIEDVFSISGRGT VVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +VKVG+VEVEIVGI+ T KTT TGVEMFRK L++G AG+NVGVLLRGTK++E+ERG VL K
Sbjct: 236 IVKVGEEVEIVGIKTTKTTCTGVEMFRKLLDEGRAGENVGVLLRGTKRDEIERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360
      PGSI PH FE E+YVLSKEEGGRHTPFF YRPQFY RTT DVTGSI LPEGVEMVMPGD
Sbjct: 296 PGSIHPHTTFESEVYVLSKEEGGRHTPFFKGYRPQFYFRTT DVTGSIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      N+K+TV LL P+A+ G +FAIREGGRTVGAGVVS ++
Sbjct: 356 NIKMTVTLIHPIAMADGLRFAIREGGRTVGAGVVS 393

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tr Q6FZC0 Elongation factor tu (EF-tu) [tuf1] [Bartonella quintana] 391 AA  
Q6FZC0\_BARQU (Rochalimaea quintana)]

align

Score = 555 bits (1429), Expect = e-157

Identities = 277/399 (69%), Positives = 322/399 (80%), Gaps = 8/399 (2%)

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Query: 1 MAKEKENRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK KE RT PHVNIGTIGHV HGKT+L+AAI+ K E K YD ID AP+E+ RG
Sbjct: 1 MAKSKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEERARG 55

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120
      ITI+T+H+EYETE RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI
Sbjct: 56 ITISTAHVEYETEKRYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 115

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP IVVFLNK S Y+FPGDD PIV GSAL ALE
Sbjct: 116 LLARQVGVPPIVFLNKVDQVDDAEELLELEIRELLSKYDFPGDDPIVKGSAALAALE 175

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240
      + K ++GE + V LM+EVD+YIPTPER ++ FL+P+EDVFSI+GRGT VVTGR+ERG
Sbjct: 176 D-KDKSIGE--DAVRLLMSEVDNYIPTPERPVDQPFLLPIEDVFSISGRGT VVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      V+KVG+E+ET+GIR T KTTVTGVEMFRK L++G+AGDN+G LLRG +E +ERG VL K
Sbjct: 233 VIKVGEEIEIIGIRPTSKTTVTGVEMFRKLLDQGGAGDNIGALLRGVDREGIERGQVLAK 292

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360
      PGS+TPH +F+ E Y+L+K+EGGRHTPFFTNYRPQFY RTT DVTG +TLPEG+EMVMPGD
Sbjct: 293 PGSVTPHTRFKAAYILTKDEGGRTHTPFFTNYRPQFYFRTT DVTGIVTLPEGIEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 399

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NV + V LI P+A+E +FAIREGGRTVGAG+VS IIE  
 Sbjct: 353 NVAMDVSLIVPIAMEEKLRF AIREGGRTVGAGIVSKIIE 391

tr Q5WZL4 Elongation factor Tu [tufA] [Legionella pneumophila 396  
 Q5WZL4\_LEGPL (strain Lens)] AA  
align

Score = 555 bits (1429), Expect = e-157  
 Identities = 277/400 (69%), Positives = 323/400 (80%), Gaps = 5/400 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAKEKE R PHVN+GTIGHV HGKTTL+AAI+ +++ K K YD ID AP+E+ERG  
 Sbjct: 1 MAKEKFERKKPHVNVGTIGHVDHGKTTLTAAITTIMAKKYGGTAKAYDQIDAAPEERERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI+T+H+EYE+ +RHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI  
 Sbjct: 61 ITISTAHVEYESASRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LLSRQVGVP+IVVF+NK S+Y+FPGDD FL+ GSAL+ALE  
 Sbjct: 121 LLSRQVGVPYIVVFMNKADMVDDPELLELVEMEVRDLLSSYDFPGDDIPIVGSALKALE 180

Query: 181 EAKAGNVGEWGEKVL-KLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIER 239  
 G + G K + KL+ +DSYIF P R+ +K FL+P+EDVFSI+GRGTVVTGR+E  
 Sbjct: 181 ----GEDSDIGVKAIEKLVTMSYIPEPVRNIDKPFLLPIEDVFSISGRGTVVTGRVES 236

Query: 240 GVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLC 299  
 G+VKVG+EVEIVGIR TQKTT TGVEMFRK L++G AGENVGVLLRGTK++EVERG VL  
 Sbjct: 237 GIVKVGEEVEIVGIRDTQKTTCTGVEMFRKLLDEGRAGDNVGVLLRGTKRDEVERGQVLA 296

Query: 300 KPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPOFYVRTTDTG SITLPEGVEMVMPG 359  
 KPG+I PH KEE E+YVLSKEEGGRHTPFF YRQFY RTTDTG+ LP GVEMVMPG  
 Sbjct: 297 KPGTIKPHTKFEAEVYVLSKEEGGRHTPFFNGYRPOFYFRTTDTGTCDLPSGVEMVMPG 356

Query: 360 DNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 DNV++ V L +P+A++ G +FAIREGGRTVGAGV+ IIE  
 Sbjct: 357 DNVQLVVS LHAPIAMDEGLRFAIREGGRTVGAGVVAKIIE 396

sp Q925Y6 Elongation factor Tu (EF-Tu) [tufA] [Rhizobium meliloti 391 AA  
 EFTU\_RHIME (Sinorhizobium meliloti)]  
align

Score = 554 bits (1428), Expect = e-156  
 Identities = 276/399 (69%), Positives = 320/399 (80%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAK KF R PHVNIGTIGHV HGKT+L+AAI+ K E K YD ID AP+EK RG  
 Sbjct: 1 MAKSKFERNKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEEKARG 55

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 120  
 ITI+T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI  
 Sbjct: 56 ITISTAHVEYETPNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSAADGMPQTREHI 115

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP IVVFLNK S+Y+EPGDD PIV GSAL ALE  
 Sbjct: 116 LLARQVGVPPIVFLNKVDQVDDAELLELEVELEIRELLSSYEFPGDDIPIVKGSAALALE 175

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240  
 ++ +GE + + +LMA VD+YIPTPER ++ FIMP+EDVFSI+GRGT VVTGR+ERG  
 Sbjct: 176 DSDK-KIGE--DAIRELMAAVDAYIPTPERPIDQPFLMPIEDVFSISGRGT VVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGT KKEEVERGMVLCK 300  
 +VKVG+E+EI+GIR T KTT TGVEMFRK L++G+AGDN+G LLRG + VERG +LCK  
 Sbjct: 233 IVKVGEEIEIVGIRPTTKTTCTGVEMFRKLLDQGGAGDNIGALLRGVDRNGVERGQILCK 292

Query: 301 PGSITPHKKFEEIEYVLSKEEGGRHTPFFTNYRPFYVRTT DVTGSITLPEGVEMVMPGD 360  
 PGS+ PH+KF+ E Y+L+KEEGGRHTPFFTNYRPFY RTTDTG +TLPEG EMVMPGD  
 Sbjct: 293 PGSVKPHRKFKAEAYILTKEEGGRHTPFFTNYRPFYFRTT DVTGIVTLPEGTEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NV + VELI P+A+E +FAIREGGRTVGAG+V+I+E  
 Sbjct: 353 NVTVDVELIVPIAMEEKLRF AIREGGRTVGAGIVASIVE 391

tr Q6FZL2 Elongation factor tu (EF-tu) [tuf2] [Bartonella quintana 391 AA  
 Q6FZL2\_BARQU (Rochalimaea quintana)]

align

Score = 554 bits (1428), Expect = e-156

Identities = 277/399 (69%), Positives = 322/399 (80%), Gaps = 8/399 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF RT PHVNIGTIGHV HGKT+L+AAI+ K E K YD ID AP+E+ RG  
 Sbjct: 1 MAKSKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAP EERARG 55

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI+T+H+EYETE RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 56 ITISTAHVEYETEK RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 115

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP IVVFLNK S Y+EPGDD PIV GSAL ALE  
 Sbjct: 116 LLARQVGVPPIVFLNKVDQVDDAELLELEVELEIRELLSKYDFPGDDIPIVKGSAALALE 175

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240  
 + K ++GE + V LM+EV D+YIPTPER ++ EL+P+EDVFSI+GRGT VVTGR+ERG  
 Sbjct: 176 D-KDSIGE--DAVRLLMSEVDNYIPTPERPIDQPFLPIEDVFSISGRGT VVTGRVERG 232

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGT KKEEVERGMVLCK 300  
 V+KVG+E+EI+GIR T KTTVTGVEMFRK L++G+AGDN+G LLRG +E +ERG VL K  
 Sbjct: 233 VIKVGEEIEIIGIRPTS KTTVTGVEMFRKLLDQGGAGDNIGALLRGVDREGIERGQVLAK 292

Query: 301 PGSITPHKKFEEIEYVLSKEEGGRHTPFFTNYRPFYVRTT DVTGSITLPEGVEMVMPGD 360  
 PGS+TPH +F+ E Y+L+K+EGGRHTPFFTNYRPFY RTTDTG +TLPEG+EMVMPGD  
 Sbjct: 293 PGSVTPHTRFKAEAYILTKDEGGRTHTPFFTNYRPFYFRTT DVTGIVTLPEGIEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NV + V LI P+A+E +FAIREGGRTVGAG+VS IIE  
 Sbjct: 353 NVAMDVSLIVPIAMEEKLRF AIREGGRTVGAGIVSKIIE 391

tr Q7MYE8 Elongation factor Tu (EF-Tu) [tufA] [Photorhabdus 394  
 Q7MYE8\_PHOLL luminescens AA  
 (subsp. laumondii)] align

Score = 554 bits (1428), Expect = e-156  
 Identities = 269/398 (67%), Positives = 321/398 (80%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 M+KEKE RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D LIDAP+EK RG  
 Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGNARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI+TSH+EY+T +RHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGMPQTREHI  
 Sbjct: 61 ITISTSHVEYDTPSRHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LL RQVGVP+I+VFLNK S Y+FFGDDTP++ GSAL+ALE  
 Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELEVMEVRELLSQYDFPGDDTPVIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVVGRIERG 240  
 EW K+++L +DSYIP PER ++ FL+P+EDVFSI+GRGTVVVGRI+ERG  
 Sbjct: 181 -----GDAWEAKIIEALAEALDSYIPEPERAIDQPFLLPIEDVFSISGRGTVVVGRIERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 +VVKVG+EVEIVGI+ T KTT TGVMFRK L++G AG+NVGVLLRGTK++E+ERG VL K  
 Sbjct: 236 IVKVGEEVEIVGIKDTTKTTCTGVMFRKLLDEGRAGENVGVLLRGTKRDEIERGQVLAK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360  
 PGSI PH FE E+Y+LSK+EGGRHTPEE YRPQFY RTTDTVGS+I LPEGVEMVMPGD  
 Sbjct: 296 PGSIKPHTTFESEVYILSKDEGGRHTPFFKGYRPFYFRTTDTVGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398  
 N+++ V LI+P+A++ G +FAIREGGRTVGAGVV+ +I  
 Sbjct: 356 NIQMKVTLIAPIAMDQGLRFAIREGGRTVGAGVVAKVI 393

sp P18668 Elongation factor Tu (EF-Tu) [tuf] [Synechococcus sp. 409  
 EFTU\_SYNP6 (strain PCC AA  
 6301) (Anacystis nidulans)] align

Score = 554 bits (1427), Expect = e-156  
 Identities = 278/409 (67%), Positives = 328/409 (79%), Gaps = 10/409 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MA+ KE RT PH NIGTIGHV HGKTTL+AAI+ VL+ G+A+ + Y +ID AP+EK RG  
 Sbjct: 1 MARAKFERTKPHANIGTIGHVDHGKTTLTAAITTVLAKAGMAKARAYADIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 61 ITINTAHVEYETGNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
 LL++QVGVP+IVVFLNK S+Y+FFGDD PIVAGSAL+ALE  
 Sbjct: 121 LLAKQVGVPNIIVFLNKEDMVDDAEELLELEVRELLSSYDFPGDDIPVAGSALQALE 180

Query: 181 EAKAGNVGE-----WGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTG 235  
 + G G+ W +K+LKLM EVD+YIPTPER+ ++ FLM VEDVF+I GRGTV TG  
 Sbjct: 181 AIQGGASGQKGDNPWVDKILKLMEEVDAYIPTPEREVD RPFLMAVEDVFTITGRGT VATG 240

Query: 236 RIERGVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERG 295  
 RIERG VKVG+ +EIVG+R T+ TTVTGVEMF+K L++G AGDNVG+LIRG +K ++ERG  
 Sbjct: 241 RIERGSVKVGETIEIVGLRDTRSTTVTGVEMFQKTLDEGLAGDNVGLLLRGIQKTDIERG 300

Query: 296 MVLCKPGSITPHKKFEE EIIYVLSKEEGGRHTPFFTNYRPPQFYVRTT DVTGSI---TLPEG 352  
 MVL KPGSITPH KFE E+YVL KEEGGRHTPEF YRPQFYVRTT DVTG+I T +G  
 Sbjct: 301 MVLAKPGSITPHTKFES EYVVLKKEEGGRHTPFFPGYRPPQFYVRTT DVTGAISDFTADDG 360

Query: 353 --VEMVMPGDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 EMV+PGD +K+TVELI+P+A+E G +FAIREGGRT+GAGVVS I++  
 Sbjct: 361 SAAEMVIPGDRIKMTVELINPIAIEQGMRF AIREGGRTIGAGVVS KILQ 409

sp O31297 Elongation factor Tu (EF-Tu) [tuf] [Buchnera aphidicola] 394  
 EFTU\_BUCAI (subsp. AA  
 Acyrthosiphon pisum) (Acyrtosiphon pisum symbiotic align  
 bacterium)]

Score = 554 bits (1427), Expect = e-156  
 Identities = 270/398 (67%), Positives = 319/398 (79%), Gaps = 5/398 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKD YDNIDNAPQEKERG 60  
 M+KEKF R PH+N+GTHGV NGKTTL+AAI+ VLS K + +D IDNAP+EK RG  
 Sbjct: 1 MSKEKFQRLKPHINVGTIGHVDHGKTTLTAAITTVLSKKFGGSARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVS AADGMPQTREHI 120  
 ITI TSH+RY+TE RHYAHVDCPGHADY+KNMITGAAQMDGAILVV+A DGMPQTREHI  
 Sbjct: 61 ITINTSHVEYDTEFRHYAHVDCPGHADYIKNMITGAAQMDGAILVVAATDGMPQTREHI 120

Query: 121 LLSRQVGVP H I VFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFP GDDTPIVAGSALRALE 180  
 LL RQVGVP+I+VFINK + Y+FP GDDTPI+ GSAL+ALE  
 Sbjct: 121 LLGRQVGVPYII VFLNKC D MVDDEELLELVEMEVRDLLTQYDFPGDDTPIIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLM AEVDSYIPTPERDTEKTF LMPVEDVFSIAGRGT VVTGRIERG 240  
 EW K++ L +DSYIP F+R ++ FL+F+EDVFSI+GRGT VVTGR+E+G  
 Sbjct: 181 GDP-----EWESKIIDL SKFLDSYIPEPKRAVDQPFLLPIEDVFSISGRGT VVTGRVEKG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 ++KVG+EVEIVGI+ T NTT TGVEMFRK L++G AG+NVGVLLRGTK++E+ERG VL K  
 Sbjct: 236 IIKVGEEVEIVGIKTTKTTCTGVEMFRKLLDEGRAGENVGVLLRGTKRDEIERGQVLAK 295

Query: 301 PGSITPHKKFEE EIIYVLSKEEGGRHTPFFTNYRPPQFYVRTT DVTGSI TLPEGVEMVMPGD 360  
 PCSI PH FE E+YVLSKEEGGRHTPEF YRPQFY RTT DVTGSI LPEG+EMVMPGD  
 Sbjct: 296 PGSIHPTTFESEYVLSKEEGGRHTPFFKGYRPPQFYFR TTDVTGSIELPEGIEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 398  
 N+K+TV LI+P+A+ G +FAIREGGRTVGAGVVS ++  
 Sbjct: 356 NIKMTVTLINPIAMADGLRFAIREGGRTVGAGVVS KVL 393

sp P33165 Elongation factor Tu (EF-Tu) [tuf] [Bacteroides fragilis] 394 AA

EFTU\_BACFR

align

Score = 553 bits (1426), Expect = e-156

Identities = 271/399 (67%), Positives = 317/399 (78%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MAKEKE RT PHVNIGTIGHV HSKTTL+AAI+ VL+ KGL+E++ +D+IDNAP+EKERG  
 Sbjct: 1 MAKEKFERTKPHVNIGTIGHVDHGKTTLTAAITTVLAKKGLSELRSFDSIDNAPEEKERG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI TSH+EYET RHYAHVDCPGHADVKNM+TGAAQMDGAI+VV+A DGMPQTREHI  
 Sbjct: 61 ITINTSHVEYETANRHYAHVDCPGHADVKNMVTGAAQMDGAIIVVAATDGPMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQV VP +VVF+NK S Y+F GD+TPI+ GSAL AL  
 Sbjct: 121 LLARQVNVPKLVVFMNKCMDVEDAEMLLEVEMRELLSFYDFDGDNTPIIQGSALGALN 180

Query: 181 EAKAGNVGEWGEKVLKMAEVD SYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTGRIERG 240  
 V +W +KV++LM VD++IP P RD +K FLMPVEDVEST GRGTV TGRLE G  
 Sbjct: 181 -----GVEKWEDKVMELMEAVDTWIPLPPRDVDKPFMLPVEDVFSITGRGT VATGRIETG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
 V+ VGDE+EI+G+ +K+ VTGVEMFRK L++GEAGDNVG+LLRG K E++RGMVLCK  
 Sbjct: 236 VIHVGDEIEILGLGEDKKS VVTGVEMFRKLLDQGEAGDNVGLLLRGVDKNEIKRGMVLCK 295

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTT DVTGSITLPEGVEMVMPGD 360  
 PG I PH KF+ E+Y+L KEEGGRHTPE YRPQFY+RT D TG ITLPEG ENVMPGD  
 Sbjct: 296 PGQIKPHSKFKA EYIILKKEEGGRHTPFHNKYRPQFYLR TMDCTGEITLPEGTEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NV ITVELI EVAL +G +FAIREGGRTVGAG ++ II+  
 Sbjct: 356 NVTITVELIYPVALNIGLRFAIREGGRTVGAGQITEIID 394

sp P33171 Elongation factor Tu (EF-Tu) [tuf] [Synechococcus sp. 409  
 EFTU\_SYNP7 (strain PCC AA  
 7942) (Anacystis nidulans R2)] align

Score = 553 bits (1424), Expect = e-156

Identities = 277/409 (67%), Positives = 328/409 (79%), Gaps = 10/409 (2%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
 MA+ KE RT PH NIGTIGHV HSKTTL+AAI+ VL+ G+A+ + Y +ID AP+EK RG  
 Sbjct: 1 MARAKFERTKPHANIGTIGHVDHGKTTLTAAITTVLAKAGMAKARAYADIDAAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI T+H+EYET RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI  
 Sbjct: 61 ITINTAHVEYETGNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVPPIVFLNXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+QVGVP+IVVFLNK S+Y+FPGDD PIVAGSAL+ALE  
 Sbjct: 121 LLAKQVGVPNIVVFLNKEDMVDDAELELLEVELEVRELLSSYDFPGDDIPIVAGSALQALE 180

Query: 181 EAKAGNVGE-----WGEKVLKMAEVD SYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTG 235  
 + G G+ W +K+LKLM EVD+YIPTPER+ ++ FLM VEDVF+I GRGTV TG  
 Sbjct: 181 AIQGGASGQKGNPWVDKILKLMEEVDAYIPTPEREVD RPFLMAVEDVFTITGRGT VATG 240

Query: 236 RIERGVVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERG 295  
RIERG VKVG+ +EIVG+R T+ TTVTGVEMF+K L++G AGDNVG+ILRG +K ++ERG  
Sbjct: 241 RIERGSVKVGETIEIVGLRDRSTRSTTVTGVEMFQKTLDEGLAGDNVGLLLRGIQKTDIERG 300

Query: 296 MVLCKPGSITPHKKFEEEIYVLSKEEGGRHTPFFFTNYRPOFYVRTTDTVTSI---TLPEG 352  
MVL KPGSITPH KFE E+YVL K+EGGRHTPEF YRPQFYVRTTDTVTSI T +G  
Sbjct: 301 MVLAKPGSITPHTKFESEVYVLKKDEGGRHTPFFPGYRPOFYVRTTDTVTAISDFTADDG 360

Query: 353 --VEMVMPGDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
EMV+EGD +K+TVELL+P+A+E G +FAIREGGRT+GAGVVS I++  
Sbjct: 361 SAAEMVIPGDRIKMTVELINPIAIEQGMRFIREGGRTIGAGVVSILQ 409

sp Q8ZAN8 Elongation factor Tu-B (EF-Tu-B) [tufB] [Yersinia pestis] 394 AA  
EFTU2\_YERPE

align

Score = 553 bits (1424), Expect = e-156  
Identities = 271/399 (67%), Positives = 319/399 (79%), Gaps = 5/399 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60  
M+KEKE RT PHVN+GTIGHV HGKTTL+AAI+ VL+ + +D IINAP+EK RG  
Sbjct: 1 MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGSARAFDQIDNAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQOTREHI 120  
ITI TSH+EX+T RHYAHVDCPGHADVKNMITGAAQMDGAILVV+A DGPMPQOTREHI  
Sbjct: 61 ITINTSHVEYDTPARHYAHVDCPGHADVKNMITGAAQMDGAILVVAATDGPMPQOTREHI 120

Query: 121 LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180  
LL RQVGVP+I+VELNK S Y+FPGDTP++ GSAL+ALE  
Sbjct: 121 LLGRQVGVPYIIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPVIRGSALKALE 180

Query: 181 EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240  
EW K+++L +DSYIP PER ++ FL+P+EDVFSI+GRGTVVTGR+ERG  
Sbjct: 181 -----GDAEWEAKIIEALAEALDSYIPQPERAIDRPFLLPIEDVFSISGRGTVVTGRVERG 235

Query: 241 VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300  
+VVKVG+EVEIVGI T KTT TGVEMFRK L++G AG+NVGVLLRGTK+++V+RG VL K  
Sbjct: 236 IVKVGEEVEIVGIIDTIKTCTGVEMFRKLLDEGRAGENVGVLLRGTKRDDVQRGQVLAK 295

Query: 301 PGSITPHKKFEEEIYVLSKEEGGRHTPFFFTNYRPOFYVRTTDTVTSITLPEGVEMVMPGD 360  
PGSI PH KFE E+Y+LSK+EGGRHTPEF YRPQFY RTTDTVTSI LPEGVEMVMPGD  
Sbjct: 296 PGSIKPHTKFESEVYILSKDEGGRHTPFFKGYRPOFYFRTTDTVGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
NV + V LI+P+A++ G +FAIREGGRTVGAGVV+ +IE  
Sbjct: 356 NVNMVNLIAPIAMDDGLRFAIREGGRTVGAGVVAKVIE 394

tr Q66FQ9 Elongation factor Tu [tufA] [Yersinia  
Q66FQ9\_YERPS pseudotuberculosis]

394  
AA  
align

Score = 553 bits (1424), Expect = e-156



Identities = 271/399 (67%), Positives = 319/399 (79%), Gaps = 5/399 (1%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        M+KEKF RT PHVN+GTIGHV HGKTTL+AAI+ VL+      + +D IDNAP+EK RG
Sbjct: 1  MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGSARAFDQIDNAPEEKARG 60

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI TSH+EY+T RHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI
Sbjct: 61  ITINTSHVEYDTPARHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LL RQVGVP+I+VFLNK                               S Y+FPGDDT++ GSAL+ALE
Sbjct: 121  LLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRLLSQYDFPGDDTPVIRGSALKALE 180

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
        EW K+++L +DSYTP PER ++ FL+P+EDVFSI+GRGTVVTGR+ERG
Sbjct: 181  -----GDAEWEAKIIELAEALDSYIPQPERAIDRPFLPIEDVFSISGRGTVVTGRVERG 235

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        +VVKVG+EVEIVGI T KTT TGVEMFRK L++G AG+NVGVLLRGTK+++V+RG VL K
Sbjct: 236  IVKVGEEVEIVGIIDTIKTTCTGVEMFRKLLDEGRAGENVGVLRLGTRKDDVQRGQVLAK 295

Query: 301  PGSITPHKKFEEIIYVLSKEEGGRHTPFFFTNYRPQFYVRTTDTVGSITLPEGVEMVMPGD 360
        PGSI PH KFE E+Y+LSK+EGGRHTFFF YRPQFY RTTDTVGS+I LPEGVEMVMPGD
Sbjct: 296  PGSIKPHTKFESEVYIILSKDEGGRHTPFFKGYPQFYFRTTDTVGTIELPEGVEMVMPGD 355

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
        NV + V LI+P+A++ G +FAIREGGRTVGAGV+ +IE
Sbjct: 356  NVNMVNLIAPIAMDDGLRFAIREGGRTVGAGVAKVIE 394

```

tr Q8KHX9            **Elongation factor TU (EF-Tu) [tufB] [Bartonella henselae 391 AA**  
Q8KHX9\_BARHE    **(Rochalimaea henselae)]**

align

Score = 552 bits (1423), Expect = e-156

Identities = 278/399 (69%), Positives = 320/399 (79%), Gaps = 8/399 (2%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
        MAK KF RT PHVNIGTIGHV HGKT+L+AAI+      K   E K YD ID AP+E+ RG
Sbjct: 1  MAKSKFERTKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGEFKAYDQIDAAPEERARG 55

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
        ITI+T+H+EYETE RHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI
Sbjct: 56  ITISTAHVEYETEKRYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 115

Query: 121  LLSRQVGVPPIVFLNKXXXXXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180
        LL+RQVGVP IVVFLNK                               S Y+FPGDD PIV GSAL ALE
Sbjct: 116  LLARQVGVPPIVFLNKVDQVDDAEELLELEVRELLSKYDFPGDDIPVKGSALE 175

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVTGRIERG 240
        + K ++GE + V LM+EVD+YIPTPER ++ FLMP+EDVFSI+GRGTVVTGR+ERG
Sbjct: 176  D-KDKSIGE--DAVRLLMSEVDNYIPTPERPVDQPFLLPIEDVFSISGRGTVVTGRVERG 232

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
        V+KVG+EVEI+GIR T KTTVTGVEMFRK L++G+AGDN+G LLRG +E +ERG VL K

```

Sbjct: 233 VIKVGEEVEIIGIRPTSKTTVTGVMFRKLLDQGQAGDNIGALLRGIDREGIERGQVIAK 292

Query: 301 PGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGVSITLPEGVEMVMPGD 360  
 P S+TPH +P+ E Y+L+K+EGGRHTPFFTNYRPQFY RTTENTG +TLPEG EMVMPGD

Sbjct: 293 PASVTPHTRFKAEAYILTKDEGGRHTPFFTNYRPQFYFRTTDTGIVTLPEGTEMVMPGD 352

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 NV + V LI P+A+E +FAIREGGRTVGAG+VS IIE

Sbjct: 353 NVAMDVSLIVPIAMEEKLRFIREGGRTVGAGIVSKIIE 391

tr Q89J82 Elongation factor TU [tuf] [Bradyrhizobium japonicum] 396 AA  
Q89J82\_BRAJA

align

Score = 552 bits (1423), Expect = e-156  
 Identities = 276/401 (68%), Positives = 321/401 (79%), Gaps = 7/401 (1%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60  
 MAK KF R PH NIGTIGHV HGKT+L+AAI+ +L+ G A YD ID AP+EK RG

Sbjct: 1 MAKAKFERNKPHCNIGTIGHVDHGKTSLTAAITKILAETGGATFTAYDQIDKAPEEKARG 60

Query: 61 ITIATSHIEYETETRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120  
 ITI+T+H+EYET+ RHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI

Sbjct: 61 ITISTAHVEYETKNRHYAHVDCPGHADVKNMITGAAQMDGAILVVSADGMPQTREHI 120

Query: 121 LLSRQVGVP HIVVFLNKXXXXXXXXXXXXXXXXXXXXX SAYEFPGDDTPIVAGSALRALE 180  
 LL+RQVGVP +VVFLNK S YEFPGD PI+ GSAL ALE

Sbjct: 121 LLARQVGVPALVVFLNKCDMVDDPELLELVELEVRELLSKYEFPGDKIPIIKGSALAALE 180

Query: 181 EA--KAGNVGEWGEKVLKLMAEVD SYIPTPERDTEKTFMLPVEDVFSIAGRGT VVTGRIE 238  
 ++ K G+ + +L+LM VD YIP PER ++ ELMFVEDVESI+GRGT VVTGR+E

Sbjct: 181 DSDKKLGH-----DAILELMRNVDEYIPQPERPIDQPFMLPVEDVFSISGRGT VVTGRVE 235

Query: 239 RGVVKGDEVEIVGIRATQKTTVTGVMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVL 298  
 RG+VKG+E+EIVG+RATQKTTVTGVMFRK L++G+AGDN+G LLRGTK+E+VERG VL

Sbjct: 236 RGIVKVGEEIEIVGLRATQKTTVTGVMFRKLLDQGQAGDNIGALLRGTKREDVERGQVL 295

Query: 299 CKPGSITPHKKFEEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDTGVSITLPEGVEMVMP 358  
 KPGS+ PH KT+ E Y+L+KEEGGRHTPFFTNYRPQFY RTTDTG + LPEG EMVMP

Sbjct: 296 AKPGSVKPHTKFKAEAYILTKEEGGRHTPFFTNYRPQFYFRTTDTGVVHLPEGTEMVMP 355

Query: 359 GDNVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399  
 GDN+ + V LI P+A+E +FAIREGGRTVGAGV++IIE

Sbjct: 356 GDNIAEVHLIVPIAMEEKLRFIREGGRTVGAGVVASIIE 396

tr Q727D5 Translation elongation factor Tu [tuf] [Desulfovibrio] 397.  
Q727D5\_DESVH vulgaris AA  
 (strain Hildenborough / ATCC 29579 / NCIMB 8303)] align

Score = 552 bits (1423), Expect = e-156  
 Identities = 271/399 (67%), Positives = 319/399 (79%), Gaps = 2/399 (0%)

Query: 1 MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60

```

Sbjct: 1      M KEKF R PHVNIGTIGH+ HGKTTL+AAI+      L G +      YD ID AP+EKERG
               MGKEKFERKKPHVNIGTIGHIDHGKTTLTAAITKTAGLLQGKFIAAYDEIDKAPEEKERG 60

Query: 61      ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
               ITIAT+H+EYET TRHYAHVDCPGHADY+KNMITGAAQMDGAI+VV+A DGPMPQTREHI

Sbjct: 61      ITIATAHVEYETATRHYAHVDCPGHADYIKNMITGAAQMDGAIIVVAATDGPMPQTREHI 120

Query: 121     LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
               LL+RQVGVP+IVVFLNK                      +-Y FEGDD P+V GSAL+ALE

Sbjct: 121     LLARQVGVPYIIVVFLNKCDMVDDEELLELVELEVRELLTSYGFPGDDVPVVRGSALKALE 180

Query: 181     EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
               + + + + +L+A DSYIF P+RD +K FLMP+EDVFSI+GRGTVVTGR+ERG

Sbjct: 181     SDDPNS--DACKPIRELLAACDSYIPEPQRDIDKPFMLPIEDVFSISGRGTVVTGRVERG 238

Query: 241     VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
               V+KVG+EVEIVGI+ T K+T TGVEMFRK L++G+AGDN+G LLRG K+++VERG VL

Sbjct: 239     VIKVGEEVEIVGIKDTTKSTCTGVEMFRKLLDQGGAGDNIGALLRGVVKRDDVERGQVLAA 298

Query: 301     PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
               P SEEPH+KF+ E+YVLSKEEGGRHTPEF+ YRPQFY RTTD+TG ITL EGVEMVMPGD

Sbjct: 299     PKSITPHRKFAEVYVLSKEEGGRHTPFSSGYRPFYFRTTDITGVITLEEGVEMVMPGD 358

Query: 361     NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNIIE 399
               N      VELI+P+A+ELG +FAIREGGRTVGAGVVS I+E

Sbjct: 359     NATFNVELIAPIAMELGRLFAIREGGRTVGAGVVSEIVE 397

```

```

tr Q7N9B1      Translation elongation factor EF-Tu.B [tufB]      394
Q7N9B1_PHOLL  [Photorhabdus luminescens (subsp. laumondii)]  AA
                                                    align

```

Score = 552 bits (1422), Expect = e-156  
Identities = 268/398 (67%), Positives = 320/398 (80%), Gaps = 5/398 (1%)

```

Query: 1      MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPQEKERG 60
               M+KEKF R PHVN+GTIGHV HGKTTL+AAI+ VL+      + +D IDNAP+EK RG

Sbjct: 1      MSKEKFERKKPHVNVGTIGHVDHGKTTLTAAITTVLAKTFGGNARAFDQIDNAPEEKARG 60

Query: 61      ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
               ITI+TSH+EY+T +RHYAHVDCPGHADYVKNMITGAAQMDGAILVV+A DGPMPQTREHI

Sbjct: 61      ITISTSHVEYDTPSRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHI 120

Query: 121     LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
               LL RQVGVP+I+VFLNK                      S Y+FPGDDTF++ GSAL+ALE

Sbjct: 121     LLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRLLSQYDFPGDDTPVIRGSALKALE 180

Query: 181     EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFMLPVEDVFSIAGRGTVVTGRIERG 240
               EW K++L +DSYIP PER ++ FL+P+EDVFSI+GRGTVVTGR+ERG

Sbjct: 181     -----GDAEWEAKIIEALDSYIPEPERAIDQPFLPIEDVFSISGRGTVVTGRVERG 235

Query: 241     VVKVGDEVEIVGIRATQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
               +VVKVG+EVEIVGI+ T KTF TGVEMFRK L++G AG+NVGVLLRGTK++E+ERG VL K

Sbjct: 236     IVKVGEEVEIVGIKDTTKTTCTGVEMFRKLLDEGRAGENGVLLRGTKRDEIERGQVLAK 295

Query: 301     PGSITPHKKFEEIIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360

```

```

PGST PR FE E+Y+LSK+EGGRATPEE YRPQFY RTTDVGTG+I LPEGVEMVMPGD
Sbjct: 296 PGSIKPHTTFESEVYILSKDEGGRHTPFFFKGYRPQFYFRTTDVGTIELPEGVEMVMPGD 355

Query: 361 NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 398
      N+++ V LI+P+A++ G +FAIREGGRTVGAGVV+ +I
Sbjct: 356 NIQMKVTLIAPIAMDQGLRFAIREGGRTVGAGVVAKVI 393

```

```

sp Q8UE16      Elongation factor Tu (EF-Tu) [tufA] [Agrobacterium      391
  EFTU_AGRT5  tumefaciens
               (strain C58 / ATCC 33970)]
               align

```

Score = 551 bits (1421), Expect = e-156  
 Identities = 274/399 (68%), Positives = 320/399 (79%), Gaps = 8/399 (2%)

```

Query: 1  MAKEKFNRTNPHVNIGTIGHVYHGKTTLSAAISAVLSLKGLAEMKDYNIDNAPQEKERG 60
      MAK KF R PHVNIGTIGHV HGKT+L+AAL+ K E K YD TD AP+EK RG
Sbjct: 1  MAKSKFERNKPHVNIGTIGHVDHGKTSLTAAIT-----KYFGFEKAYDQIDAAPEEKARG 55

Query: 61  ITIATSHIEYETETRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGMPQTREHI 120
      ITL+T+H+EYET RHYAHVDCPGHADYVKNMITGAAQMDGAILV SAADGMPQTREHI
Sbjct: 56  ITISTAHVEYETPARHYAHVDCPGHADYVKNMITGAAQMDGAILVCSAADGMPQTREHI 115

Query: 121  LLSRQVGVPPIVVFLNKXXXXXXXXXXXXXXXXXXXXXSAYEFPGDDTPIVAGSALRALE 180
      LL+RQVGVP IVVFLNK S+Y+FPQDD PI+ GSAL ALE
Sbjct: 116  LLARQVGVPPIVVFLNKVDQVDDAELELLEVELEVRELLSSYDFPGDDIPIIKGSALAALE 175

Query: 181  EAKAGNVGEWGEKVLKLMAEVDSYIPTPERDTEKTFILMPVEDVFSIAGRGTVVVTGRIERG 240
      ++ +GE + + +LMA VD+YIPTER ++ FILMP+EDVFSI+GRGTVVVTGR+ERG
Sbjct: 176  DSDK-KIGE--DAIRELMAAVDAYIPTPERPIDQPFLMPIEDVFSISGRGTVVVTGRVERG 232

Query: 241  VVKVGDEVEIVGIRATQKTTVTGVMERKELEKGEAGDNVGVLLRGTKKEEVERGMVLCK 300
      +VKVG+EVEIVGIR T KTTVTGVMERK L+*G+AGDN+G L+RG ++ VERG +LCK
Sbjct: 233  IVKVGEEVEIVGIRPTSKTTVTGVMERKLLDQGGAGDNIGALVRGVTRDGVERGQILCK 292

Query: 301  PGSITPHKKFEEIEYVLSKEEGGRHTPFFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGD 360
      PGS+ PHKKF E Y+L+KEEGGRHTPFFFTNYRPQFY RTTDVGTG ++LPEG EMVMPGD
Sbjct: 293  PGSVKPHKKFMAEAYILTKEEGGRHTPFFFTNYRPQFYFRTTDVTGIVSLPEGTEMVMPGD 352

Query: 361  NVKITVELISPVALELGTKFAIREGGRTVGAGVVSNI 399
      NV + VELL P+A+E +FAIREGGRTVGAG+V++I+E
Sbjct: 353  NVTVEVELIVPIAMEEKLRFIREGGRTVGAGIVASIVE 391

```

Database: EXPASY/UniProtKB

Posted date: Jun 6, 2005 10:37 AM

Number of letters in database: 640,866,274

Number of sequences in database: 1,974,938

```

Lambda      K      H
0.315      0.135    0.383

```

```

Gapped
Lambda      K      H
0.267      0.0410   0.140

```

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
length of query: 399  
length of database: 640,866,274  
effective HSP length: 128  
effective length of query: 271  
effective length of database: 388,074,210  
effective search space: 105168110910  
effective search space used: 105168110910  
T: 11  
A: 40  
X1: 16 ( 7.3 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 42 (22.0 bits)  
S2: 75 (33.5 bits)

Wallclock time: 18 seconds

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